

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 16:14:01; Search time 1405.95 Seconds  
(without alignments)  
8816.891 Million cell updates/sec

Title: US-10-681-972-12  
Perfect score: 286  
Sequence: 1 ggggaattcgatcccaagaaa.....taataaggatccgaattccc 286

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
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- 30: em\_htg\_hum.\*
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- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_fod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	286	100.0	286	6	AR014689	AR014689 Sequence
2	286	100.0	286	6	AR432389	AR432389 Sequence
3	269.2	94.1	270	6	AR014691	AR014691 Sequence
4	269.2	94.1	270	6	AR432391	AR432391 Sequence
5	216.6	75.7	500	6	AR014686	AR014686 Sequence
6	216.6	75.7	500	6	AR432386	AR432386 Sequence
7	190.8	66.7	308	6	AR014682	AR014682 Sequence
8	190.8	66.7	308	6	AR432382	AR432382 Sequence
9	186.6	65.2	451	8	BNUS9459	U59459 Brassica na
10	186.2	65.1	475	8	RSEFP3	X97319 R.sativus m
11	179.8	62.9	414	6	E31545	E31545 Antibacteri
12	179.8	62.9	414	8	AB012871	AB012871 Wasabia j
13	178.8	62.5	395	8	RSU18557	U18557 Raphanus sa
14	178.8	62.5	414	6	A26875	A26875 R.sativus A
15	178.8	62.5	414	6	A39549	A39549 Sequence 37
16	178.8	62.5	414	6	A63404	A63404 Sequence 19
17	178.8	62.5	414	6	AR050153	AR050153 Sequence
18	178.8	62.5	414	6	AR130272	AR130272 Sequence
19	178.8	62.5	414	6	I23728	I23728 Sequence 48
20	178.8	62.5	414	6	AR207337	AR207337 Sequence
21	178.8	62.5	414	6	AR374914	AR374914 Sequence
22	178.4	62.4	363	8	AF528180	AF528180 Brassica
23	178.2	62.3	416	6	E31546	E31546 Antibacteri
24	177.4	62.0	243	6	BD174927	BD174927 Disease t
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26	176.6	61.7	403	6	A68845	A68845 Sequence 13
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29	176.2	61.6	400	6	A68647	A68647 Sequence 15
30	176.2	61.6	454	8	AY063779	AY063779 Arabidops
31	175.8	61.5	243	6	BD174928	BD174928 Disease t
32	175	61.2	288	6	A39553	A39553 Sequence 41
33	175	61.2	288	6	AR050161	AR050161 Sequence
34	175	61.2	288	6	AR130280	AR130280 Sequence
35	175	61.2	288	6	I23736	I23736 Sequence 58
36	174.2	60.9	243	6	AX412329	AX412329 Sequence
37	174.2	60.9	243	6	AX412502	AX412502 Sequence
38	174.2	60.9	243	6	AX507351	AX507351 Sequence
39	174.2	60.9	243	6	AX590057	AX590057 Sequence
40	174.2	60.9	274	8	AY133787	AY133787 Arabidops
41	172.2	60.2	285	6	AR014692	AR014692 Sequence
42	172.2	60.2	285	6	AR432392	AR432392 Sequence
43	171	59.8	243	6	AX412406	AX412406 Sequence
44	171	59.8	243	6	AX412601	AX412601 Sequence
45	171	59.8	243	6	AX651878	AX651878 Sequence

ALIGNMENTS

RESULT 1  
AR014689  
LOCUS  
DEFINITION Sequence 12 from patent US 5773696.  
ACCESSION AR014689  
VERSION AR014689.1 GI:3972143  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 286)  
AUTHORS Liang,J., Shah,D.Maganlal, Wu,Y.Shun. and Rosenberger,C.Annette.  
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi  
JOURNAL Patent: US 5773696-A 12 30-JUN-1998;

AR014689 286 bp DNA linear PAT 05-DEC-1998

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Best Local Similarity 100.0%; Pred. No. 1.9e-71; Indels 0; Gaps 0;
Matches 286; Conservative 0; Mismatches 0;

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DB 1 GGGAAATTCGGATCCCAAGAAAGTAATAGATATGGCTAAAGTTTGTCTACCAATCATCTCTCTTC 60

QY 61 TCTTTGCTGCTCTTGTCTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGGT 120
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QY 121 TGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCATGCAGGA 180
DB 121 TGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCATGCAGGA 180

QY 181 ACCAATGCAGAAACCTTGAAGAGCAGAAACACGGATCTTGCACACTATGTCTTCCAGCTC 240
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QY 241 ACAATGTAATTTGTTACTTCCCATGTTAATAAGGATCCGAATTCOC 286
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RESULT 2
LOCUS AR432389 286 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6653280.
ACCESSION AR432389
VERSION AR432389.1 GI:40194666
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 286)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 12-25-NOV-2003;
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Best Local Similarity 100.0%; Pred. No. 1.9e-71; Indels 0; Gaps 0;
Matches 286; Conservative 0; Mismatches 0;

QY 1 GGGAAATTCGGATCCCAAGAAAGTAATAGATATGGCTAAAGTTTGTCTACCAATCATCTCTCTTC 60
DB 1 GGGAAATTCGGATCCCAAGAAAGTAATAGATATGGCTAAAGTTTGTCTACCAATCATCTCTCTTC 60

QY 61 TCTTTGCTGCTCTTGTCTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGGT 120
DB 61 TCTTTGCTGCTCTTGTCTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGGT 120

QY 121 TGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCATGCAGGA 180
DB 121 TGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCATGCAGGA 180

QY 181 ACCAATGCAGAAACCTTGAAGAGCAGAAACACGGATCTTGCACACTATGTCTTCCAGCTC 240
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QY 241 ACAATGTAATTTGTTACTTCCCATGTTAATAAGGATCCGAATTCOC 286
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DB 241 ACAATGTAATTTGTTACTTCCCATGTTAATAAGGATCCGAATTCOC 286

RESULT 3
LOCUS AR014691 270 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 14 from patent US 5773696.
ACCESSION AR014691
VERSION AR014691.1 GI:3972145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 270)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic
fungi
JOURNAL Patent: US 5773696-A 14-30-JUN-1998;
FEATURES             Location/Qualifiers
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Best Local Similarity 99.3%; Pred. No. 1.3e-66; Indels 0; Gaps 0;
Matches 268; Conservative 2; Mismatches 0;

QY 9 GGATCCAAAGAAAGTAATAGATATGGCTAAAGTTTGTACCATCATCTCTCTCTTTGCT 68
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QY 69 GCTCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGTTGCGAG 128
DB 61 GCTCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGTTGCGAG 120

QY 129 AGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGC 188
DB 121 AGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGC 180

QY 189 AGAAACCTTGAAGAGCAGAAACACGGATCTTGCACACTATGTCTTCCAGCTCACAATGT 248
DB 181 AGAAACCTTGAAGAGCAGAAACACGGATCTTGCACACTATGTCTTCCAGCTCACAATGT 240

QY 249 ATTCTGTTACTTCCCATGTTAATAAGATCC 278
DB 241 ATTCTGTTACTTCCCATGTTAATAAGATCC 270

RESULT 4
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DEFINITION Sequence 14 from patent US 6653280.
ACCESSION AR432391
VERSION AR432391.1 GI:40194668
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 270)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 12-25-NOV-2003;
FEATURES             Location/Qualifiers
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ORIGIN
Query Match          94.1%; Score 269.2; DB 6; Length 270;
Best Local Similarity 99.3%; Pred. No. 1.3e-66;
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Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 69 GCTCTGTTCTCTTTGCTGCTTTGAAGCACCACAAATGGTGGATGCAAGTTGTGCGAG 128
Db 61 GCTCTGTTCTCTTTGCTGCTTTGAAGCACCACAAATGGTGGATGCAAGTTGTGCGAG 120
QY 129 AGACCAAGTGGACATGCTCAGAGTTTGTGGAGCAACAAATGCATGCAGGAACCAATGC 188
Db 121 AGACCAAGTGGACATGCTCAGAGTTTGTGGAGCAACAAATGCATGCAGGAACCAATGC 180
QY 189 AGAAACCTTGAAGAGCAGAACACGGATCTTGAACATATGCTTCCAGCTCACAATGT 248
Db 181 AGAAACCTTGAAGAGCAGAACACGGATCTTGAACATATGCTTCCAGCTCACAATGT 240
QY 249 ATTGTTACTTCCAGTTTAATAGATCC 278
Db 241 ATTGTTACTTCCAGTTTAATAGATCC 270

RESULT 5
LOCUS AR014686 500 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 9 from patent US 5773696.
ACCESSION AR014686
VERSION AR014686.1 GI:3972140
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 500)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 9 30-JUN-1998;
FEATURES Location/Qualifiers
source 1..500
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ORIGIN
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Best Local Similarity 91.6%; Pred. No. 1.8e-51;
Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

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Db 50 ATCCAGAAAGTAATAGATATGCTAAGTTTGCTACCATCATCTCTCTCTTTGCTGC 109
QY 71 TCTGTTCTCTTTGCTGCTTTGAAGCACCACAAATGGTGGATGCA--AGGTTGTGCGA 127
Db 110 TCTGTTCTCTTTGCTGCTTTGAAGCACCACAAATGGTGGATGCAAGTTGTGCGA 169
QY 128 GAGACCAAGTGGACATGCTCAGAGTTTGTGGAGCAACAAATGCATGCAGGAACCAATG 187
Db 170 GAGTCCAAGTGGACATGCTCAGAGTTTGTGGAGCAACAAATGCATGCAGGAACCAATG 229
QY 188 CAGAAACCTTGAAGAGCAGAACACGGATCTTGAACATATGCTTCCAGCTCACAATG 247
Db 230 CAGAAACCTTGAAGAGCAGAACACGGATCTTGAACATATGCTTCCAGCTCACAATG 289
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RESULT 7
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DEFINITION Sequence 5 from patent US 5773696.
ACCESSION AR014682
VERSION AR014682.1 GI:3972136
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 308)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 5 30-JUN-1998;
FEATURES Location/Qualifiers
source 1..308
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Best Local Similarity 86.1%; Pred. No. 4.9e-44;
Matches 223; Conservative 0; Mismatches 33; Indels 3; Gaps 1;

QY 11 ATCCAGAAAGTAATAGATATGCTAAGTTTGCTACCATCATCTCTCTCTTTGCTGC 70
Db 50 ATCCAGAAAGTAATAGATATGCTAAGTTTGCTACCATCATCTCTCTCTTTGCTGC 109
QY 71 TCTGTTCTCTTTGCTGCTTTGAAGCACCACAAATGGTGGATGCA--AGGTTGTGCGA 127

RESULT 6
LOCUS AR432386 500 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6653280.

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ACCESSION AR432386
VERSION AR432386.1 GI:40194663
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 500)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide AlyAPP from Alysum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 9 25-NOV-2003;
FEATURES Location/Qualifiers
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Db 290 TATTGTTACTTCCCATGTTAAT 312

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RESULT 7
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DEFINITION Sequence 5 from patent US 5773696.
ACCESSION AR014682
VERSION AR014682.1 GI:3972136
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 308)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 5 30-JUN-1998;
FEATURES Location/Qualifiers
source 1..308
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Best Local Similarity 86.1%; Pred. No. 4.9e-44;
Matches 223; Conservative 0; Mismatches 33; Indels 3; Gaps 1;

QY 11 ATCCAGAAAGTAATAGATATGCTAAGTTTGCTACCATCATCTCTCTCTTTGCTGC 70
Db 50 ATCCAGAAAGTAATAGATATGCTAAGTTTGCTACCATCATCTCTCTCTTTGCTGC 109
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ORIGIN
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Best Local Similarity 84.3%; Pred. No. 7.2e-41;
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QY 90 TTGAGACACCAACATGGTGATGC---AGTTTGGGAGAGACCAAGTGGGACATGG 146
Db 61 TTGAGACACCAACATGGTGGAGGCGAGAGTTGTGGGAGAGTCAAGTGGGACATGG 120
QY 147 TCAGGAGTTTGTGGGACCAACATGCATGCAGCAACCAATGCAGAACCTTGAAGAGCA 206
Db 121 TCAGGAGTTTGTGGGACCAACATGGTGGGAGAGTCAAGTGGGACATGCATGCAGAACCTTGAAGAGCA 180
QY 207 GAACACGGATCTTGCACATATCTTCTCCAGCTCACAATGTATTTGTATTTCCATCT 266
Db 181 CGACATGGATCTTGCACATATCTTCTCCATATCTTCCATATCAGAGTATCTGTACTTCCATCT 240
QY 267 TAATAGGATCGAA 281
Db 241 TAATATTCTACAA 255

RESULT 13
RSU18557
LOCUS
DEFINITION
Raphanus sativus antifungal protein 1 preprotein (Rs-APP1) mRNA,
complete cds.
U18557
ACCESSION
U18557.1 GI:644773
VERSION
KEYWORDS
SOURCE
Raphanus sativus (radish)
Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
1 (sites)
Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,
Osborn,R.W., Kester,A., Rees,S.B., Torrekens,S., Van Leuven,F.,
Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.
Small cysteine-rich antifungal proteins from radish: their role in
host defense
Plant Cell 7, 568-573 (1995)
2 (bases 1 to 395)
Terras,F.R.
Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylan 42,
Heverlee, Belgium, B-3001
On Feb 9, 1995 this sequence version replaced gi:609321.
LOCATION/Qualifiers
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/mol_type="mRNA"
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REFERENCE
AUTHORS
Raphanus sativus (radish)
Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
1 (bases 1 to 414)
Broekaert,W.F., Cammue,B.P.A., Terras,F.R.G., Vanderleyden,J.,
Osborn,R.W. and Rees,S.B.
BIOCIDAL PROTEINS
Patent: WO 9305153-A 33 18-MAR-1993;

RESULT 14
A26875
LOCUS
DEFINITION
R.sativus APP1 gene.
ACCESSION
A26875
VERSION
A26875.1 GI:1247352
KEYWORDS
SOURCE
Raphanus sativus (radish)
Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
1 (bases 1 to 414)
Osborn,R.W. and Rees,S.B.
BIOCIDAL PROTEINS
Patent: WO 9305153-A 33 18-MAR-1993;

Query Match 62.5%; Score 178.8; DB 8; Length 395;
Best Local Similarity 84.3%; Pred. No. 1.4e-40;
Matches 214; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
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REFERENCE
AUTHORS
Raphanus sativus (radish)
Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
1 (bases 1 to 414)
Osborn,R.W. and Rees,S.B.
BIOCIDAL PROTEINS
Patent: WO 9305153-A 33 18-MAR-1993;

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Search completed: May 18, 2004, 17:59:03  
Job time : 1407.95 secs

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D <sub>b</sub>	66	TTTTTGCTGCTTTTCTGAAGCACCAACAATGTTGGAAGCACAGAAGTTGTGCGAAGAGGCCAACG	12
Qy	137	TGGGCATGCTCAGGAGTTTGTGGGAACAACAATGATGCGAGGAACCAATGCGAGAAACCT	19
D <sub>b</sub>	126	TGGGCATGCTCAGGAGTCTGTGGAAACAATAACGCATGCAAGANTCAGTGCAATTAACT	18
Qy	197	TGAAGAGCAGAACACGGATCTTGGCAACTATGCTCTCCAGCTCAAAATGTAATTTGTTA	25
D <sub>b</sub>	186	TGAAGAAGCACCATGGAATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTA	24

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RESULT 15
ACCESSION A39549
LOCUS A39549
DEFINITION Sequence 37 from Patent WO9416076.
ACCESSION A39549
VERSION A39549.1
KEYWORDS GI:2295842
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 414)
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL Patent: WO 9416076-A 37 21-JUL-1994;
ZENECA LTD (GB)
COMMENT Other publication AU 5820494 940815.
FEATURES
    source
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            /organism="unidentified"
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[illegible]

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 16:12:26 ; Search time 278.85 Seconds  
(without alignments)  
4357.126 Million cell updates/sec

Title: US-10-681-972-12  
Perfect score: 286  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: Geneseqn2002as:\*  
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8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	256.8	89.8	481	2	AAT99289
4	216.6	75.7	500	2	AAT94581
5	190.8	66.7	308	2	AAT94577
6	179.8	62.9	414	3	AAT94577
7	178.8	62.5	414	2	AAT94577
8	178.8	62.5	414	2	AAT94577
9	178.8	62.5	414	2	AAT94577
10	178.8	62.5	414	2	AAT94577
11	178.2	62.3	416	3	AAT94577
12	177.4	62.0	243	6	ABQ82690
13	176.6	61.7	403	2	AAV10632
14	176.2	61.6	400	2	AAV10632
15	175.8	61.5	243	6	ABQ82691
16	175	61.2	261	2	AAQ38652
17	175	61.2	288	2	AAQ70130
18	174.2	60.9	243	6	ABZ14241
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20	172.6	60.3	394	9	ADA68378
21	171	59.8	243	7	ADA68378
22	169.4	59.2	426	9	ADC51223
23	167	58.4	575	3	AAZ99339

24	166	58.0	449	3	AAZ53190	Raphanus
25	155	54.2	1973	3	AAZ45924	Arabidops
26	120.8	42.2	1616	2	AAV10646	A. thalia
27	116.2	40.6	606	3	AAZ99326	DNA encod
28	115.4	40.3	522	3	AAZ99324	DNA encod
29	115.4	40.3	534	3	AAZ51396	Portion o
30	115.4	40.3	534	3	AAZ99327	DNA encod
31	115.4	40.3	534	3	AAZ99325	DNA encod
32	112.4	39.3	243	9	ADC87758	DNA encod
33	111.6	39.0	306	2	AAT94580	Cloned 3'
34	111.6	39.0	437	3	AAZ99331	DNA encod
35	110	38.5	443	3	AAZ99330	DNA encod
36	109	38.1	485	3	AAZ99337	DNA encod
37	108.6	38.0	485	3	AAZ99333	DNA encod
38	107.4	37.6	434	3	AAZ99332	DNA encod
39	107.4	37.6	446	3	AAZ99329	DNA encod
40	107.4	37.6	485	3	AAZ99335	DNA encod
41	107.4	37.6	488	3	AAZ99338	DNA encod
42	107.4	37.6	557	3	AAZ99336	DNA encod
43	104.8	36.6	1093	3	AAZ99334	DNA encod
44	76.8	26.9	284	2	AAQ38651	Truncated
45	76.8	26.9	284	2	AAQ70129	Antimicro

ALIGNMENTS

RESULT 1  
AAT94574  
ID AAT94574 standard; cDNA; 286 BP.  
XX  
AC AAT94574;  
XX  
DT 12-MAY-1998 (first entry)  
XX  
DE Alyssum species anti-fungal polypeptide AlyAFP cDNA sequence.  
XX  
KW Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;  
XX phytopathogenic fungus; resistance; ss.  
XX  
OS Alyssum sp.  
XX  
FH Key Location/Qualifiers  
CDS 117..269  
FT /\*tag= a  
FT /product= "mature AlyAFP protein"  
FT /note= "no start codon given at 5' end of sequence"  
XX  
PN WO9737024-A2.  
XX  
PD 09-OCT-1997.  
XX  
PF 27-MAR-1997; 97WO-US005709.  
XX  
PR 29-MAR-1996; 96US-00627706.  
XX (MONS ) MONGANTO CO.  
XX  
PI Liang J, Shah D, Wu Y, Rosenberger CA;  
XX  
DR WPI; 1997-503109/46.  
DR P-PSDB; AAW35558.  
XX  
PT Alyssum antifungal polypeptide and corresponding DNA - used in the  
PT production of transgenic plants resistant to phytopathogenic fungi.  
XX  
PS Claim 12; Page 68; 92pp; English.  
XX  
CC This sequence encodes the mature protein of an antifungal polypeptide  
CC (AlyAFP) isolated from plants of the genus Alyssum. The sequence was PCR  
CC amplified using primers AAT94583-194584, and the resultant 264 bp  
CC fragment was cloned as a BamHI fragment into the expression vector  
CC pMON23317 to generate plasmid pMON22652. The AlyAFP sequence in this

CC plasmid is placed under control of an E35S promoter and the maize HSP70  
 CC intron 1 sequence. The protein can be used to control phytopathogenic  
 CC fungi, whilst the DNA can be used to produce transgenic plants that  
 CC express the protein making them resistant to the phytopathogenic fungi  
 XX  
 SQ Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 286; DB 2; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-81; Mismatches 0; Indels 0; Gaps 0;  
 Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAAATCGGATCCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTTC 60  
 Db 1 GGGAAATCGGATCCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTTC 60  
 QY 61 TCTTTGCTGCTCTTTCT 120  
 Db 61 TCTTTGCTGCTCTTTCT 120  
 QY 121 TGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCGATGCGAG 180  
 Db 121 TGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCGATGCGAG 180  
 QY 181 ACCAATGCGAGAAACCTTGAAGAGCAGACACGATCTTTGCAACTATGCTTTCCAGCTC 240  
 Db 181 ACCAATGCGAGAAACCTTGAAGAGCAGACACGATCTTTGCAACTATGCTTTCCAGCTC 240  
 QY 241 ACAATGATTTTGTACTTCCCATGTTAATAAGGATCCGAATCCC 286  
 Db 241 ACAATGATTTTGTACTTCCCATGTTAATAAGGATCCGAATCCC 286

## RESULT 2

AAT94582  
 ID AAT94582 standard; DNA; 270 BP.

XX AC AAT94582;

XX 12-MAY-1998 (first entry)

XX Amplified Alysum species antifungal polypeptide gene from pMON22652.

XX Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;  
 XX phytopathogenic fungus; resistance; ss.

XX Alysum sp.

XX Key Location/Qualifiers  
 XX CDS 22..261

FT sig\_peptide /product= "AlyAFP antifungal polypeptide"  
 FT /tag= a  
 FT 22..108  
 FT /tag= b  
 FT mat\_peptide 109..258  
 FT /tag= c

XX WO9737024-A2.

XX 09-OCT-1997.

XX 27-MAR-1997; 97WO-US005709.

XX 29-MAR-1996; 96US-00627706.

XX (MONS ) MONSANTO CO.

XX Liang J, Shah D, Wu Y, Rosenberger CA;

XX WPI; 1997-503109/46.

XX P-PSDB; AAW35560.

XX Alysum antifungal polypeptide and corresponding DNA - used in the  
 PT production of transgenic plants resistant to phytopathogenic fungi.

XX Example 4; Page 69; 92pp; English.  
 PS  
 XX This sequence represents the cDNA sequence cloned into the E. coli  
 CC cassette vector pMON2317 to generate vector pMON22652. The cDNA encodes  
 CC the antifungal polypeptide AlyAFP, isolated from plants of the genus  
 CC Alysum. The AlyAFP polypeptide can be used to control phytopathogenic  
 CC fungi, whilst the coding DNA can be used to produce transgenic plants  
 CC that express the polypeptide making them resistant to the phytopathogenic  
 CC fungi.

XX SQ Sequence 270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;

Query Match 94.1%; Score 269.2; DB 2; Length 270;

Best Local Similarity 99.3%; Pred. No. 1.1e-75;

Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATCCAAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTCTCTTGT 68

Db 1 GGATCCAAASAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTCTCTTGT 60

QY 69 GCTCTTGTCTCTTGTCTGCTTGAAGCAGCAACAATGGTGGATGCAAGTTGTGCGAG 128

Db 61 GCTCTTGTCTCTTGTCTGCTTGAAGCAGCAACAATGGTGGATGCAAGTTGTGCGAG 120

QY 129 AGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCGATGCAAGTTGTGCGAG 188

Db 121 AGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCGATGCAAGTTGTGCGAG 180

QY 189 AGAAACCTTGAAGAGCAGACACGATCTTTGCAACTATGCTTTCCAGCTCACAATGT 248

Db 181 AGAAACCTTGAAGAGCAGACACGATCTTTGCAACTATGCTTTCCAGCTCACAATGT 240

QY 249 ATTGTTACTTCCCATGTTAATAAGGATCC 278

Db 241 ATTGTTACTTCCCATGTTAATAAGGATCC 270

## RESULT 3

AAT99289  
 ID AAT99289 standard; DNA; 481 BP.

XX AC AAT99289;

XX 12-MAY-1998 (first entry)

XX Alysum species AlyAFP cDNA sequence.

XX Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;  
 XX phytopathogenic fungus; resistance; ss.

XX Alysum sp.

XX Key Location/Qualifiers  
 XX CDS 53..292

FT sig\_peptide /product= "AlyAFP antifungal polypeptide"  
 FT /tag= a  
 FT 53..139  
 FT /tag= b  
 FT mat\_peptide 140..289  
 FT /tag= c  
 FT polyA\_signal 439..443  
 FT /tag= d

XX WO9737024-A2.

XX 09-OCT-1997.

XX 27-MAR-1997; 97WO-US005709.

XX 29-MAR-1996; 96US-00627706.

XX (MONS ) MONSANTO CO.

PT	Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi.
XX	
PS	Example 4; Page 67; 92pp; English.
XX	
CC	This sequence represents the cDNA sequence encoding the antifungal polypeptide AlyAFP, from plants of the genus Alyssum. The sequence represents a composite of the sequences isolated by 5' and 3' RACE (Rapid Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
XX	
SQ	Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;
	Query Match 75.7%; Score 216.6; DB 2; Length 500;
	Best Local Similarity 91.6%; Pred. No. 9.2e-59;
	Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY	11 ATCCAGAAAGTAATAGATATGCTAAGTGTTCACCATCATCTCTCTCTTTGGTGC 70
Db	50 ATCACAAAGTAATAGATATGCTAAGTGTCTTCATCATCTCCCTGTGCTCTGTGTC 109
QY	71 TCTTGTTCTCTTTGCTGCCCTTTGAAGCACCACAATGGTGGATGCA--AGGTTGTGCGA 127
Db	110 TCTTGTTCTCTTTGCTGCTTTGAAGCACACAGCAATGGTGAGTCACGGAAATTGTGCGA 169
QY	128 GAGACCAAGTGGACATGTCAGAGTTTTGTGGGAACAACAANTGCATGCAGGAACCAATG 187
Db	170 GATGCCAAGTGGAACATGFTGCAGCGGTGTGTGGGAATAATAAGCATGCAGGAACCAATG 229
QY	188 CAGAAACCTTTGAAGAGCAGAAACCGGATCTTGCAACTATGTCTTCCCAGCTCACAATG 247
Db	230 CAGAAACCTTTGAAGAGCAGAAACCGGATCTTGCAACTATGTCTTCCCAGCTCACAATG 289
QY	248 TATTGTACTTCCCATGTTAAAT 270
Db	290 TATTGTACTTCCCATGTTAAAT 312
RESULT 5	
AAT94577	

XX	AAT94577;	
XX	AC	
XX		
XX	12-MAY-1998	(first entry)
XX		
XX	Cloned 5' region of antifungal polypeptide cDNA.	
XX		
XX	Antifungal polypeptide; AlyAPP; inhibition; transgenic plants;	
KW	phytopathogenic fungus; resistance; ss.	
XX		
XX	Alyssum sp.	
OS		
XX		
XX	WO9737024-A2.	
PN		
XX		
XX	09-OCT-1997.	
PD		
XX		
XX	27-MAR-1997;	97MO-US005709.
PF		
XX		
XX	29-MAR-1996;	96US-00627706.
XX		
XX	(MONS ) MONSANTO CO.	
PA		
XX		
XX	Liang J, Shah D, Wu Y, Rosenberger CA;	
PI		
XX		
XX	WPI; 1997-503109/46.	
DR		
XX		
XX		
XX	Alyssum antifungal polypeptide and corresponding DNA - used in the	
PT	production of transgenic plants resistant to phytopathogenic fungi.	
PT		
XX		
XX	Example 4; Page 65; 92bp; English.	
PS		

XX This sequence is the product of the amplification of the 5' region of the  
 CC antifungal polypeptide AlyAPP, isolated from plants of the genus *Alyssum*,  
 CC by a 5' RACE (Rapid Amplification of cDNA Ends) using primers AAR94575-  
 CC T94576). The AlyAPP polypeptide can be used to control phytopathogenic  
 CC fungi, whilst the coding DNA can be used to produce transgenic plants  
 CC that express the polypeptide making them resistant to the phytopathogenic  
 CC fungi  
 XX  
 SQ Sequence 308 BP; 78 A; 71 C; 78 G; 79 T; 0 U; 2 Other;

Query Match 66.7%; Score 190.8; DB 2; Length 308;  
 Best Local Similarity 86.1%; Pred. No. 1.3e-50;  
 Matches 223; Conservative 0; Mismatches 33; Indels 3; Gaps 1;  
 QY 11 ATCCAGAAAGTAATAGATATGCTTAAGTTTGTACCATCATCTCTCTCTTTGCTGC 70  
 DB 50 ATCAGAGAAAGTAATAGATATGCTTAAGTTTGTCTTCCATCATCTCTCTCTGCTGC 109  
 QY 71 TCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGTTGGATGCA--AGTTTGTGCGA 127  
 DB 110 TCTTGTCTCTTTGCTGCTTTTGAAGCACCACCAATGTTGGATGCA--AGTTTGTGCGA 169  
 QY 128 GAGACCAAGTGGGACATGTCAGGATTTGTGGGACCAACAAATGATGACGAAACCAATG 187  
 DB 170 GAGTCCAAGTGGGACATGTCAGGATTTGTGGGACCAACAAATGATGTCGCAAGATCAGTG 229  
 QY 188 CAGAACCTTGAAGAGCAGACACGGATCTTGCACATATGCTTCCAGCTCACAATG 247  
 DB 230 CATTAACCTTGAAGAGCAGACACGGATCTTGCACATATGCTTCCAGCTCACAATG 289  
 QY 248 TATTTGTTACTTCCCATGT 266  
 DB 290 CATATGCTACTTCCCATGT 308

RESULT 6  
 AAZ39123  
 ID AAZ39123 standard; cDNA to mRNA; 414 BP.  
 XX  
 AC AAZ39123;  
 XX  
 DT 15-SEP-2003 (revised)  
 DT 01-MAR-2000 (first entry)  
 XX  
 DE Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:1.  
 XX  
 KW Wasabia japonica; antibacterial; food additive; ds.  
 XX  
 OS Eutrema wasabi.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..243  
 FT /\*tag= a  
 FT /product= "antibacterial protein"  
 XX  
 FN JP1133678-A.  
 XX  
 PD 16-NOV-1999.  
 XX  
 PF 30-APR-1998; 98JP-00121303.  
 XX  
 PR 30-APR-1998; 98JP-00121303.  
 XX  
 PA (IWAT-) IWATE KEN.  
 XX  
 DR WPI; 2000-057353/05.  
 DR P-PSDB; AAY57564.  
 XX  
 PT An antibacterial protein gene of *Wasabia japonica* - useful as a food- or  
 PT feed-additive.  
 XX  
 PS Claim 3; Page 12-13; 16pp; Japanese.

XX The present sequence encodes an antibacterial protein isolated from  
 CC *Wasabia japonica*. The antibacterial protein can be used as a food or feed  
 CC additive. (Updated on 15-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;  
 XX  
 Query Match 62.9%; Score 179.8; DB 3; Length 414;  
 Best Local Similarity 84.3%; Pred. No. 4.8e-47;  
 Matches 215; Conservative 0; Mismatches 37; Indels 3; Gaps 1;  
 QY 30 ATGGCTAAGTTTGTACCATCATCTCTCTCTTTGCTGCTCTTGTCTCTTCTGCTGCC 89  
 DB 1 ATGGCTAAGTTTGTCT 60  
 QY 90 TTTGAAGCACCACCAATGTTGGATGC---AAGTTTGTGCGAGAGACCAAGTGGGACATGG 146  
 DB 61 TTTGAAGCACCACCAATGTTGGATGC---AAGTTTGTGCGAGAGACCAAGTGGGACATGG 120  
 QY 147 TCAGAGATTTGCGAACAACATGTCATGCGAGAACCAATGCGAGAACCAATGCGAGAAC 206  
 DB 121 TCAGAGATTTGCGAACAACATGTCATGCGAGAACCAATGCGAGAACCAATGCGAGAAC 180  
 QY 207 GAACACGGATCTTGCACATATGCTCTTCCAGCTCACAATGATTTGTACTTCCCATGT 266  
 DB 181 CGACATGATCTTGCACATATGCTCTTCCAGCTCACAATGATTTGTACTTCCCATGT 240  
 QY 267 TAATAAGGATCCGAA 281  
 DB 241 TAATAATCTACCAA 255

RESULT 7  
 AAQ38650  
 ID AAQ38650 standard; DNA; 414 BP.  
 XX  
 AC AAQ38650;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-JUL-1993 (first entry)  
 XX  
 DE Rs-APP1 cDNA.  
 XX  
 KW *Raphanus sativus*; Brassica; Arabidopsis; Caucis; Lathyrus; Clitoria;  
 KW fungicide; bactericide; antibiotic; antifungal; gram positive;  
 KW plant disease resistance; low toxicity.  
 XX  
 OS *Raphanus sativus*.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 16..256  
 FT /\*tag= a  
 XX  
 PN W09305153-A1.  
 XX  
 PD 18-MAR-1993.  
 XX  
 PF 27-AUG-1992; 92WO-GB001570.  
 XX  
 PR 29-AUG-1991; 91GB-00018523.  
 PR 13-FEB-1992; 92GB-00003038.  
 PR 25-JUN-1992; 92GB-00013526.  
 XX  
 PA (ICIL) IMPERIAL CHEM IND PLC.  
 XX  
 PI Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;  
 PI Vanderleyden J;  
 XX  
 DR WPI; 1993-100978/12.  
 XX  
 PT Biocidal proteins isolated from seeds of plants - e.g. brassica or  
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial  
 PT diseases.







ABQ82690  
ID ABQ82690 standard; cDNA; 243 BP.  
XX  
AC ABQ82690;



Db 181 CGACATGGATCTTGCAACTATATCTTCCCATATCACAGATGATCTGTACTTCCCATGT 240

Qy 267 TAA 269

Db 241 TAA 243

RESULT 15  
ABQ82691  
ID ABQ82691 standard; cDNA; 243 BP.

AA  
DT  
XX  
DE  
02-JAN-2003 (first entry)  
Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:3.

XX	OS	Eutrema wasabi.
FT	Key	Location/Qualifiers
FT	CDS	1..243
FT		/tag= a
FT		/product= "gamma-th

PN	JF2002272292-A.
XX	
XX	
PD	24-SEP-2002.
XX	
XX	
PF	22-MAR-2001; 2001JP-00083526.
XX	
XX	
PR	22-MAR-2001; 2001JP-00083526.
XX	
XX	(IWAT-) IWATE KEN.
PA	
XX	
XX	
DR	WPI: 2002-718704/78.
DR	P-PSDB; ABF53726.
XX	
XX	
PT	A disease-resistant plant in which wasabi gamma-thionin gene is
PT	introduced, creation of the disease-resistant plant.

The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Eureka wasabi (*Wasabia japonica*) gamma-thionin protein from the present invention

Sequence 243 BP; 59 A; 55 C; 55 G; 74 T; 0 U; 0 Other;

Query Match	61.5%;	Score 175.8;	DB 6;	Length 243;
Best Local Similarity	85.6%;	Pred. No. 7.2e-46;		
Matches 208; Conservative	0;	Mismatches 32;	Indels 3;	Gaps 1;

[illegible]

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	286	100.0	286	3	US-09-103-489-12
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5	269.2	94.1	270	3	US-09-103-489-14
6	269.2	94.1	270	4	US-09-829-381D-14
7	216.6	75.7	500	1	US-08-627-706-9
8	216.6	75.7	500	3	US-09-103-489-9
9	216.6	75.7	500	4	US-09-829-381D-9
10	190.8	66.7	308	1	US-08-627-706-5
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12	190.8	66.7	308	4	US-09-829-381D-5
13	178.8	62.5	414	1	US-08-377-687-48
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15	178.8	62.5	414	4	US-08-971-982-48
16	178.8	62.5	414	4	US-09-077-951-19
17	178.8	62.5	414	4	US-09-077-948A-45
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20	175	61.2	288	3	US-08-971-982-58
21	172.2	60.2	285	1	US-08-627-706-16
22	172.2	60.2	285	3	US-09-103-489-16
23	172.2	60.2	285	4	US-09-829-381D-16
24	165.8	58.0	285	1	US-08-627-706-17
25	165.8	58.0	285	3	US-09-103-489-17
26	165.8	58.0	285	4	US-09-829-381D-17
27	112.4	39.3	243	4	US-09-732-210-11

28	111.6	39.0	306	1	US-08-627-706-8	Sequence 8, Appl
29	111.6	39.0	306	3	US-09-103-489-8	Sequence 8, Appl
30	111.6	39.0	306	4	US-09-829-381D-8	Sequence 8, Appl
31	76.8	26.9	284	1	US-08-377-687-50	Sequence 50, Appl
32	76.8	26.9	284	1	US-08-777-192-50	Sequence 50, Appl
33	76.8	26.9	284	3	US-08-971-982-50	Sequence 50, Appl
34	51	17.8	565	4	US-09-589-733C-6	Sequence 6, Appl
C 35	40	14.0	40	1	US-08-627-706-11	Sequence 11, Appl
C 36	40	14.0	40	3	US-09-103-489-11	Sequence 11, Appl
C 37	40	14.0	40	4	US-09-829-381D-11	Sequence 11, Appl
38	39.8	13.9	150	1	US-08-377-687-31	Sequence 31, Appl
39	39.8	13.9	150	1	US-08-377-687-33	Sequence 33, Appl
40	39.8	13.9	150	1	US-08-377-687-34	Sequence 34, Appl
41	39.8	13.9	150	1	US-08-777-192-31	Sequence 31, Appl
42	39.8	13.9	150	1	US-08-777-192-33	Sequence 33, Appl
43	39.8	13.9	150	1	US-08-777-192-34	Sequence 34, Appl
44	39.8	13.9	150	3	US-08-971-982-31	Sequence 31, Appl
45	39.8	13.9	150	3	US-08-971-982-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1  
US-08-627-706-12  
; Sequence 12, Application US/08627706  
; Patent No. 5773896  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yennie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles B. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. 5773896th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,706  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21(10700)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6224  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 286 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-627-706-12

Query Match 100.0%; Score 286; DB 1; Length 286;  
Best Local Similarity 100.0%; Pred. No. 9.2e-84;  
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAATTCGATCCAAAGAAAGTAATAGATATGCTAAGTTTGCTACCATCTCTCTTC 60  
|||||

Db 1 GGGAAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60  
QY 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTGCTTTGAGACACCAACAATGGTGGATGCAAGGT 120  
Db 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTGCTTTGAGACACCAACAATGGTGGATGCAAGGT 120  
QY 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCGAGGA 180  
Db 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCGAGGA 180  
QY 181 ACCAATGCGAAGACCTTGAAGAGACGAGAACACCGGATCTTGCACATATGTCTTCCAGCTC 240  
Db 181 ACCAATGCGAAGACCTTGAAGAGACGAGAACACCGGATCTTGCACATATGTCTTCCAGCTC 240  
QY 241 ACAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTC 286  
Db 241 ACAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTC 286

## RESULT 2

US-09-103-489-12

; Sequence 12, Application US/09103489

; Patent No. 6215048

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; APPLICANT: Shah, Dilip M.

; APPLICANT: Wu, Yennie S.

; APPLICANT: Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for

; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

; STREET: 700 Chesterfield Village Parkway No. 6215048th

; CITY: St. Louis

; STATE: Missouri

; COUNTRY: USA

; ZIP: 63198

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/103,489

; FILING DATE: 24-JUN-1998

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Cohen, Charles E.

; REGISTRATION NUMBER: 34,565

; REFERENCE/DOCKET NUMBER: 38-21 (10700)A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (314) 537-6224

; TELEFAX: (314) 537-6047

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 286 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-103-489-12

Query Match 100.0%; Score 286; DB 3; Length 286;  
Best Local Similarity 100.0%; Pred. No. 9.2e-84;  
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60  
Db 1 GGGAAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60  
QY 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTGCTTTGAGACACCAACAATGGTGGATGCAAGGT 120

Db 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTGCTTTGAGACACCAACAATGGTGGATGCAAGGT 120  
QY 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCGAGGA 180  
Db 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCGAGGA 180  
QY 181 ACCAATGCGAAGACCTTGAAGAGACGAGAACACCGGATCTTGCACATATGTCTTCCAGCTC 240  
Db 181 ACCAATGCGAAGACCTTGAAGAGACGAGAACACCGGATCTTGCACATATGTCTTCCAGCTC 240  
QY 241 ACAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTC 286  
Db 241 ACAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTC 286

## RESULT 3

US-09-829-381D-12

; Sequence 12, Application US/09829381D

; Patent No. 6653280

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; APPLICANT: Shah, Dilip M.

; APPLICANT: Wu, Yennie S.

; APPLICANT: Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Contro

; FILE REFERENCE: 38-21 (10700) C

; CURRENT APPLICATION NUMBER: US/09/829,381D

; CURRENT FILING DATE: 2001-04-09

; PRIOR APPLICATION NUMBER: 09/103,489

; PRIOR FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 12

; LENGTH: 286

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic PCR reaction product

US-09-829-381D-12

Query Match 100.0%; Score 286; DB 4; Length 286;  
Best Local Similarity 100.0%; Pred. No. 9.2e-84;  
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60  
Db 1 GGGAAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60  
QY 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTGCTTTGAGACACCAACAATGGTGGATGCAAGGT 120  
Db 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTGCTTTGAGACACCAACAATGGTGGATGCAAGGT 120  
QY 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCGAGGA 180  
Db 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCGAGGA 180  
QY 181 ACCAATGCGAAGACCTTGAAGAGACGAGAACACCGGATCTTGCACATATGTCTTCCAGCTC 240  
Db 181 ACCAATGCGAAGACCTTGAAGAGACGAGAACACCGGATCTTGCACATATGTCTTCCAGCTC 240  
QY 241 ACAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTC 286  
Db 241 ACAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTC 286

## RESULT 4

US-08-627-706-14

; Sequence 14, Application US/08627706

; Patent No. 5773696

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
STREET: 700 Chesterfield Village Parkway No. 5773696th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/627,706  
FILING DATE: 08/06/2004  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21(10700)A  
TELEPHONE: (314)537-6224  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-627-706-14

Query Match 94.1%; Score 269.2; DB 1; Length 270;  
Best Local Similarity 99.3%; Pred. No. 2.7e-78;  
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATCCAAAGAACTAATAGATATGGCTAAGTTGCTACCATCATCTCTCTCTTTGCT 68  
DB 1 GGATCCAAAGAACTAATAGATATGGCTAAGTTGCTACCATCATCTCTCTCTTTGCT 60  
QY 69 GCTCTTCTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGTTCTGGAG 128  
DB 61 GCTCTTCTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGTTCTGGAG 120  
QY 129 AGACCAAGTGGACATGCTCAGGAGTTTGTGGGAAACAATGATGATGCAAGTGC 188  
DB 121 AGACCAAGTGGACATGCTCAGGAGTTTGTGGGAAACAATGATGATGCAAGTGC 180  
QY 189 AGAACTTCAAGAGCAGACACGATCTTGAACCTATGCTTCCAGCTCACAATGT 248  
DB 181 AGAACTTCAAGAGCAGACACGATCTTGAACCTATGCTTCCAGCTCACAATGT 240  
QY 249 ATTTGTTACTTCCCATGTTAATAGGATCC 278  
DB 241 ATTTGTTACTTCCCATGTTAATAGGATCC 270

## RESULT 5

US-09-103-489-14  
Sequence 14, Application US/09103489  
Patent No. 6215048  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
STREET: 700 Chesterfield Village Parkway No. 6215048th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,489  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21(10700)A  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-103-489-14

Query Match 94.1%; Score 269.2; DB 3; Length 270;  
Best Local Similarity 99.3%; Pred. No. 2.7e-78;  
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATCCAAAGAACTAATAGATATGGCTAAGTTGCTACCATCATCTCTCTCTTTGCT 68  
DB 1 GGATCCAAAGAACTAATAGATATGGCTAAGTTGCTACCATCATCTCTCTCTTTGCT 60  
QY 69 GCTCTTCTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGTTCTGGAG 128  
DB 61 GCTCTTCTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGTTCTGGAG 120  
QY 129 AGACCAAGTGGACATGCTCAGGAGTTTGTGGGAAACAATGATGATGCAAGTGC 188  
DB 121 AGACCAAGTGGACATGCTCAGGAGTTTGTGGGAAACAATGATGATGCAAGTGC 180  
QY 189 AGAACTTCAAGAGCAGACACGATCTTGAACCTATGCTTCCAGCTCACAATGT 248  
DB 181 AGAACTTCAAGAGCAGACACGATCTTGAACCTATGCTTCCAGCTCACAATGT 240  
QY 249 ATTTGTTACTTCCCATGTTAATAGGATCC 278  
DB 241 ATTTGTTACTTCCCATGTTAATAGGATCC 270

## RESULT 6

US-09-829-381D-14  
Sequence 14, Application US/09829381D  
Patent No. 6653280  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control  
TITLE OF INVENTION: Plant Pathogenic Fungi  
FILE REFERENCE: 38-21(10700) C  
CURRENT APPLICATION NUMBER: US/09/829,381D  
CURRENT FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 09/103,489

; PRIOR FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 270  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid  
US-09-829-381D-14

Query Match 94.1%; Score 269.2; DB 4; Length 270;  
Best Local Similarity 99.3%; Pred. No. 2.7e-78;  
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 9 GGATCCAAAGAAAGTAATAGATATGGCTTAAGTTTGCTACCATCATCTCTCTCTCTTGGCT 68  
Db 1 GGATCCAAAGAAAGTAATAGTATGGCTTAAGTTTGCTACCATCATCTCTCTCTTGGCT 60  
QY 69 GCTCTTGTCT 128  
Db 61 GCTCTTGTCT 120  
QY 129 AGACCAAGTGGGACATGGTTCAGAGTTTCTGGGACCAACAATGCTGATGCAAGTTTGGGAG 188  
Db 121 AGACCAAGTGGGACATGGTTCAGAGTTTCTGGGACCAACAATGCTGATGCAAGTTTGGGAG 180  
QY 189 AGAAACCTTTGAAAGACGAGACGAGTCTTGCAACTATGCTCTTCCAGCTCACAATGT 248  
Db 181 AGAAACCTTTGAAAGACGAGACGAGTCTTGCAACTATGCTCTTCCAGCTCACAATGT 240  
QY 249 ATTGTGTACTTCCCATGTTAATGAAGATCC 278  
Db 241 ATTGTGTACTTCCCATGTTAATGAAGATCC 270

RESULT 7  
US-08-627-706-9  
; Sequence 9, Application US/08627706  
; Patent No. 5773696  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. 5773696th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,706  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21(10700)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6224  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 500 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; LENGTH: 500 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-627-706-9

Query Match 75.7%; Score 216.6; DB 1; Length 500;  
Best Local Similarity 91.6%; Pred. No. 5e-61;  
Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1;  
QY 11 ATCAAGAAGTAATAGATATGGCTTAAGTTTGCTACCATCATCTCTCTCTCTTGGTGC 70  
Db 50 ATCAAGAAGTAATAGATATGGCTTAAGTTTGCTACCATCATCTCTCTCTCTTGGTGC 109  
QY 71 TCTTGTCT 127  
Db 110 TCTTGTCT 169  
QY 128 GAGACCAAGTGGGACATGGTTCAGGAGTTTGGGACCAACAATGCTGATGCAAGTTTGGGAG 187  
Db 170 GAGTCCCAAGTGGGACATGGTTCAGGAGTTTGGGACCAACAATGCTGATGCAAGTTTGGGAG 229  
QY 188 CAGAAACCTTTGAAAGACGAGACGAGTCTTGCAACTATGCTCTTCCAGCTCACAATG 247  
Db 230 CAGAAACCTTTGAAAGACGAGACGAGTCTTGCAACTATGCTCTTCCAGCTCACAATG 289  
QY 248 TATTTGTACTTCCCATGTTAAT 270  
Db 290 TATTTGTACTTCCCATGTTAAT 312

RESULT 8  
US-09-103-489-9  
; Sequence 9, Application US/09103489  
; Patent No. 6215048  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. 6215048th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/103,489  
; FILING DATE: 24-JUN-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 537-6224  
; TELEFAX: (314) 537-6047  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 500 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear





CIT  
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STA

STREET: 1100 NEW YORK AVENUE, N.  
CITY: WASHINGTON  
STATE: D.C.

RESULT 15  
US-08-971-982-48  
? Sequence 48, Application US/08971982  
? Patent No. 6187904  
? GENERAL INFORMATION:  
? APPLICANT: BROEKAERT, WILLEM F.  
? CAMMIE, BRUNO P.A.  
? OSBORN, RUPERT W.  
? REES, SARAH B.  
? TERRAS, FRANKY R.G.  
? VANDERLEYDEN, JOZEF  
? TITLE OF INVENTION: BIOCIDAL PROTEINS

NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971.982  
FILING DATE: 17-No. 6187904-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002.480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SER.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 16..255  
SEQUENCE DESCRIPTION: SEQ ID NO: 48:  
US-08-971-982-48

Query Match 62.5%; Score 178.8; DB 3; Length 414;  
Best Local Similarity 84.3%; Pred. No. 9.7e-49;  
Matches 214; Conservative 0; Mismatches 37; Indels 3; Gaps 1;  
QY 20 AGTAATAGATAGCTAAGTTTGTCTACCATCATCTCTCTTTGCTGCTCTGTTCT 79  
Db 6 ATTAGTATCATGGCTAAGTTTGGTCCCATCATGGCACTCTTTTGTGCTCTGTTCT 65  
QY 80 CTTTGTGCTTTTGAAGCACCACCAATGGTGGATGCA---AGTTTGGGAGAGACCAAG 136  
Db 66 TTTTGTGCTTTTGAAGCACCACCAATGGTGGAGACACAGAGTTTGGGAAGGCCAAG 125  
QY 137 TGGGACATGCTCAGGAGTTTGTGGGAACCAACATGATGACGAGCAACCAATGCAAGAACCT 196  
Db 126 TGGGACATGCTCAGGAGTTTGTGGGAACCAACATGATGACGAGCAACCAATGCAAGAACCT 185  
QY 197 TGAAGAGCAGAACACGGAATCTTGGCAACTATGTTCCAGCTCACAATGTTATTTGTTA 256  
Db 186 TGAGAAAGCAGCAGATGATCTTGGCAACTATGTTCCAGCTCACAATGTTATTTGTTA 245  
QY 257 CTTCCCATGTTAAT 270  
Db 246 CTTTCTCTGTTAAT 259

Search completed: May 18, 2004, 19:02:18  
Job time : 59.5 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:59:12 ; Search time 263.25 Seconds  
(without alignments)  
4930.226 Million cell updates/sec

Title: US-10-681-972-12

Perfect score: 286

Sequence: 1 ggggaattcgatccaagaaa.....taataaggaatccgaattccc 286

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	286	100.0	286	9	US-09-829-381A-12
2	286	100.0	286	13	US-10-681-972-12
3	269.2	94.1	270	9	US-09-829-381A-14
4	269.2	94.1	270	13	US-10-681-972-14
5	216.6	75.7	500	9	US-09-829-381A-9
6	216.6	75.7	500	13	US-10-681-972-9
7	190.8	66.7	308	9	US-09-829-381A-5
8	190.8	66.7	308	13	US-10-681-972-5
9	178.8	62.5	414	9	US-09-759-584-48
10	178.8	62.5	414	13	US-10-388-361A-45
11	178.8	62.5	414	14	US-10-006-252A-19
12	176.6	61.7	403	9	US-09-732-561-13
13	176.2	61.6	400	9	US-09-732-561-15
14	176.2	61.6	400	9	US-09-887-576-607

15 175 61.2 288 9 US-09-759-584-58  
16 174.2 60.9 243 9 US-09-938-842A-2046  
17 174.2 60.9 243 11 US-09-938-842A-2046  
18 172.2 60.2 285 9 US-09-829-381A-16  
19 172.2 60.2 285 13 US-10-681-972-16  
20 165.8 58.0 285 9 US-09-829-381A-17  
21 165.8 58.0 285 13 US-10-681-972-17  
22 120.8 42.2 1616 9 US-09-732-561-21  
23 111.6 39.0 306 9 US-09-829-381A-8  
24 111.6 39.0 306 13 US-10-681-972-8  
25 76.8 26.9 284 9 US-09-759-584-50  
26 60.6 21.2 373 9 US-09-770-696-283  
27 51 17.8 439 15 US-10-178-449A-15  
28 51 17.8 457 15 US-10-178-449A-13  
29 51 17.8 458 15 US-10-178-449A-21  
30 51 17.8 460 15 US-10-178-449A-17  
31 51 17.8 461 15 US-10-178-449A-46  
32 51 17.8 463 15 US-10-178-449A-9  
33 51 17.8 464 15 US-10-178-449A-19  
34 51 17.8 472 15 US-10-178-449A-23  
35 51 17.8 565 12 US-10-636-396-6  
36 51 17.8 603 15 US-10-178-449A-11  
37 49.6 17.3 470 15 US-10-178-213-88  
38 48 16.8 610 15 US-10-178-449A-29  
39 48 16.8 658 15 US-10-178-449A-7  
40 47.4 16.6 529 15 US-10-178-449A-48  
41 44.8 15.7 579 15 US-10-178-449A-31  
42 44.6 15.6 501 15 US-10-178-449A-5  
43 43.6 15.2 156 15 US-10-178-449A-34  
C 44 40 14.0 40 9 US-09-829-381A-11  
C 45 40 14.0 40 13 US-10-681-972-11

## ALIGNMENTS

## RESULT 1

US-09-829-381A-12

; Sequence 12, Application US/09829381A

; Patent No. US20020144306A1

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; Shah, Dilip M.

; Wu, Yennie S.

; Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for

; Controlling Plant Pathogenic Fungi

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th

; CITY: St. Louis

; STATE: Missouri

; COUNTRY: USA

; ZIP: 63198

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/829,381A

; FILING DATE: 09-Apr-2001

; CLASSIFICATION: <Unknown>

; PRIORITY INFORMATION:

; APPLICATION NUMBER: 09/103,489

; FILING DATE: 1998-06-24

; ATTORNEY/AGENT INFORMATION:

; NAME: Cohen, Charles E.

; REGISTRATION NUMBER: 34,565

; REFERENCE/DOCKET NUMBER: 38-21 (10700)A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (314) 537-6224

TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 286 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-829-381A-12

Query Match 100.0%; Score 286; DB 9; Length 286;  
Best Local Similarity 100.0%; Pred. No. 8.7e-83;  
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTTTC 60  
DB 1 GCGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTTTC 60  
QY 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTCTTGAAGCACCACCAAAATGGTGATGCAAGT 120  
DB 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTCTTGAAGCACCACCAAAATGGTGATGCAAGT 120  
QY 121 TGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGAAACAACAATGCATGCAGGA 180  
DB 121 TGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGAAACAACAATGCATGCAGGA 180  
QY 181 ACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTCAACTATGTTCCAGCTC 240  
DB 181 ACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTCAACTATGTTCCAGCTC 240  
QY 241 ACAATGTAATTTGTTACTTCCCATGTTTAATAAGATCCGAATTCCTC 286  
DB 241 ACAATGTAATTTGTTACTTCCCATGTTTAATAAGATCCGAATTCCTC 286

## RESULT 2

US-10-681-972-12  
Sequence 12, Application US/10681972  
Publication No. US20040064850A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alysium and Methods for Controlling Plant Pathogenic Fungi  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/10/681,972  
PRIOR FILING DATE: 2003-10-09  
PRIOR APPLICATION NUMBER: US/09/829,381D  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 09/103,489  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 286  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic PCR reaction product  
US-10-681-972-12

Query Match 100.0%; Score 286; DB 13; Length 286;  
Best Local Similarity 100.0%; Pred. No. 8.7e-83;  
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTTTC 60  
DB 1 GCGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTTTC 60  
QY 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTCTTGAAGCACCACCAAAATGGTGATGCAAGT 120

DB 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTCTTGAAGCACCACCAAAATGGTGATGCAAGT 120  
QY 121 TGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGAAACAACAATGCATGCAGGA 180  
DB 121 TGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGAAACAACAATGCATGCAGGA 180  
QY 181 ACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTCAACTATGTTCCAGCTC 240  
DB 181 ACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTCAACTATGTTCCAGCTC 240  
QY 241 ACAATGTAATTTGTTACTTCCCATGTTTAATAAGATCCGAATTCCTC 286  
DB 241 ACAATGTAATTTGTTACTTCCCATGTTTAATAAGATCCGAATTCCTC 286

## RESULT 3

US-09-829-381A-14  
Sequence 14, Application US/09829381A  
Patent No. US20020144306A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF  
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/829,381A  
FILING DATE: 09-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/103,489  
FILING DATE: 1998-06-24  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-829-381A-14

Query Match 94.1%; Score 269.2; DB 9; Length 270;  
Best Local Similarity 99.3%; Pred. No. 2.6e-77;  
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTTCTTCTTCT 68  
DB 1 GGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTTCTTCTTCT 60  
QY 69 GCTCTTGTCTCTTGTCTTGTGCTCTTGAAGCACCACCAAAATGGTGATGCAAGT 128

Db 61 GCTCTTGTCTCTTTGCTGCTCTTTGAAGCACCACAAATGGTGGATGCAAGTTGTGGCG 120  
QY 129 AGACCAAGTGGGACATGTCAGGAGTTGTGGGACACAAATGATGATGAGGACCAATGC 188  
Db 121 AGACCAAGTGGGACATGTCAGGAGTTGTGGGACACAAATGATGATGAGGACCAATGC 180  
QY 189 AGAAACCTTTGAAAGAGCAGAACACGGATCTTTGCAACTATGTCCTCCAGCTCACAATGT 248  
Db 181 AGAAACCTTTGAAAGAGCAGAACACGGATCTTTGCAACTATGTCCTCCAGCTCACAATGT 240  
QY 249 ATTTGTACTTCCCATGTTAATAAGATCC 278  
Db 241 ATTTGTACTTCCCATGTTAATAAGATCC 270

## RESULT 4

US-10-681-972-14  
; Sequence 14, Application US/10681972  
; Publication No. US20040064850A1  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Contro  
; FILE REFERENCE: 38-21 (10700) C  
; CURRENT APPLICATION NUMBER: US/10/681,972  
; PRIOR FILING DATE: 2003-10-09  
; PRIOR APPLICATION NUMBER: US/09/829,381D  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/103,489  
; PRIOR FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 270  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid  
US-10-681-972-14

Query Match 94.1%; Score 269.2; DB 13; Length 270;  
Best Local Similarity 99.3%; Pred. No. 2.6e-77;  
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATCCAAAGAACTAATAGATATGGCTAAGTTGGCTACCATCATCTCTCTCTTTGCT 68  
Db 1 GGATCCAAAGAACTAATAGATATGGCTAAGTTGGCTACCATCATCTCTCTCTTTGCT 60  
QY 69 GCTCTTGTCTCTTTGCTGCTTTGAAGCACCACAAATGATGATGAGGACCAATGC 128  
Db 61 GCTCTTGTCTCTTTGCTGCTTTGAAGCACCACAAATGATGATGAGGACCAATGC 120  
QY 129 AGACCAAGTGGGACATGTCAGGAGTTGTGGGACACAAATGATGATGAGGACCAATGC 188  
Db 121 AGACCAAGTGGGACATGTCAGGAGTTGTGGGACACAAATGATGATGAGGACCAATGC 180  
QY 189 AGAAACCTTTGAAAGAGCAGAACACGGATCTTTGCAACTATGTCCTCCAGCTCACAATGT 248  
Db 181 AGAAACCTTTGAAAGAGCAGAACACGGATCTTTGCAACTATGTCCTCCAGCTCACAATGT 240  
QY 249 ATTTGTACTTCCCATGTTAATAAGATCC 278  
Db 241 ATTTGTACTTCCCATGTTAATAAGATCC 270

## RESULT 5

US-09-829-381A-9  
; Sequence 9, Application US/09829381A  
; Patent No. US20020144306A1

GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
Shah, Dilip M.  
Wu, Yonnie S.  
Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/829,381A  
FILING DATE: 09-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/103,489  
FILING DATE: 1998-06-24  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 500 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-829-381A-9

Query Match 75.7%; Score 216.6; DB 9; Length 500;  
Best Local Similarity 91.6%; Pred. No. 5e-60;  
Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 11 ATCCAGAAAGTAATAGATATGGCTAAGTTGGCTACCATCATCTCTCTCTTTGCTGC 70  
Db 50 ATCCAGAAAGTAATAGATATGGCTAAGTTGGCTACCATCATCTCTCTCTTTGCTGC 109  
QY 71 TCTTGTCTCTTTGCTGCTTTGAAGCACCACAAATGATGATGAGGACCAATGC 127  
Db 110 TCTTGTCTCTTTGCTGCTTTGAAGCACCACAAATGATGATGAGGACCAATGC 169  
QY 128 GAGACCAAGTGGGACATGTCAGGAGTTGTGGGACACAAATGATGATGAGGACCAATGC 187  
Db 170 GATCCCAAGTGGGACATGTCAGGAGTTGTGGGACACAAATGATGATGAGGACCAATGC 229  
QY 188 CAGAAACCTTTGAAAGAGCAGAACACGGATCTTTGCAACTATGTCCTCCAGCTCACAATGT 247  
Db 230 CAGAAACCTTTGAAAGAGCAGAACACGGATCTTTGCAACTATGTCCTCCAGCTCACAATGT 289  
QY 248 TATTGTACTTCCCATGTTAAT 270  
Db 290 TATTGTACTTCCCATGTTAAT 312

## RESULT 6

US-10-681-972-9  
; Sequence 9, Application US/10681972  
; Publication No. US20040064850A1

```

; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Alyssum spp
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22)-(22)
; OTHER INFORMATION: N = any nucleotide
; IS-10-681-972-9

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Query Match	75.7%;	Score	216.6;	DB	13;	Length	500;
Best Local Similarity	91.6%;	Pred.	No. Se=60;				
Matches	241;	Conservative	0;	Mismatches	19;	Indels	3;
Gaps	1						

  

QY	11	ATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTCCTTTGCTGC	70
Dd	50	ATCAGAGAAAGTAATAGATATGGCTAAGTGTCCTCCATCATCTCCCTGTCTCTCGTCGC	109
QY	71	TCTTGTTCTCTTTGCTGCTTTTGAGCACCAACAATGGTGGATGCA---AGTTTGTGGCA	127
Dd	110	TCTTGTTCTCTTTGCTGCTTTTGAAGCACCAAGAATGGTGGAGTGCAGGAAGTTGTGGCA	169
QY	128	GAGACCAAGTGGGACATGGTCAGGAGTTTGTGGAACACAACATGCCATGCAGGAACCAATG	187
Dd	170	GAGTCCAAGTGGAAATGGTCAGGCGTGTGTGGGATAATAACGCATGCAGGAACCAATG	229
QY	188	CAGAAAACCTTGAAAGAGCAGAACCGAATCTTGCAACTATGTCTTCCCAGCTCACAAAGT	247
Dd	230	CAGAAACCTTGAAGAGCAGAACCGAATCTTGCAACTATGTCTTCCCAGCTCACAAAGT	289
QY	248	TATTGTGTACTTCCCAATGTAAT	270
Dd	290	TATTGTGTACTTCCCAATGTAAT	312

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1  RESULT 7
2
3  US-09-829-381A-5
4  ; Sequence 5, Application US/09829381A
5  ; Patent No. US20020144306A1
6  ; GENERAL INFORMATION:
7  ;
8  ; APPLICANT: Liang, Jihong
9  ;          Shah, Dilip M.
10 ;          Wu, Yonnie S.
11 ;
12 ; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
13 ;                   Controlling Plant Pathogenic Fungi
14 ;
15 ; NUMBER OF SEQUENCES: 20
16 ;
17 ; CORRESPONDENCE ADDRESS:
18 ;
19 ; ADDRESSEE: Charles E. Cohen, Monsanto Company, BR4F
20 ;
21 ; STREET: 700 Chesterfield Village Parkway No. US20020144306A1a1h
22 ;
23 ; CITY: St. Louis
24 ;
25 ; STATE: Missouri
26 ;
27 ; COUNTRY: USA
28 ;
29 ; ZIP: 63198
30 ;
31 ; COMPUTER READABLE FORM:
32 ;
33 ; MEDIUM TYPE: Floppy disk
34 ;
35 ; COMPUTER: IBM PC compatible

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RESULT 10
US-10-388-361A-45
// Sequence 45, Application US/10388361A
// Publication No. US20030226169A1
// GENERAL INFORMATION:
// APPLICANT: Van Amerongen, Aart
// APPLICANT: Fant, Franky,
// APPLICANT: Borreman, Frans
// APPLICANT: De Samblanx, Genevova
// APPLICANT: Sitjtsma, Iolke
// APPLICANT: Meloen, Robbert
// APPLICANT: Puijk, Wouter
// APPLICANT: Schaeper, Wilhelmus
// APPLICANT: Broekaert, Willem
// APPLICANT: Van Gelder, Wilhelmus
// APPLICANT: Rees, Sarah
// TITLE OF INVENTION: Antifungal Proteins
// FILE REFERENCE: 50094PDDVD
// CURRENT APPLICATION NUMBER: US/10/388,361A
// CURRENT FILING DATE: 2003-03-13
// PRIOR APPLICATION NUMBER: US 09/077,948
// PRIOR FILING DATE: 1998-08-07
// PRIOR APPLICATION NUMBER: PCT/GB96/03068
// PRIOR FILING DATE: 1996-12-12
// PRIOR APPLICATION NUMBER: GB 9605552.9
// PRIOR FILING DATE: 1996-03-28
// PRIOR APPLICATION NUMBER: GB 9525455.3
// PRIOR FILING DATE: 1995-12-13
// NUMBER OF SEQ ID NOS: 141
// SOFTWARE: FastSQ for Windows Version 4.0
// SEQ ID NO 45
// LENGTH: 414
// TYPE: DNA
// ORGANISM: Raphanus sativus
US-10-388-361A-45

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Query Match	62.5%	Score 178.8;	DB 13;	Length 414;
Best Local Similarity	84.3%;	Pred. No. 9.7e-48;		
Matches 214; Conservative	0;	Mismatches 37;	Indels 3;	Gaps 1;
Qy	20	AGTAATAGATATGCTAAGTTTGCTACCATCATCTCTTCTCTTTGTGCTCTGTGTTCT	79	
Db	6	ATTAGTCATCATGGCTAAAGTTTGCGTCCATCATCGCACTCTTTTTGCTGCTCTGTGTTCT	65	
Qy	80	CTTTGCTGCCCTTTGAAGCACCACAATGGTGGATGC---AGTTGTGCAGAGACCAAG	136	
Db	66	TTTTGCTGCTTTTGAAGCACCAAATGGTGGAAAGCAGAAAGTTGTSCGAAAGGCCAAG	125	
Qy	137	TGGSACATGTGTGAGAGTCTTTGTGGGAACAACAATGCATGCAGGAACCAATGCAGAAACCT	196	
Db	126	TGGGACATGCTCAGGAGTCTGTGGAAACAATAACGCATGCAGAATCAGTGCATTAACTT	185	
Qy	197	TGAAGAGCAGACACAGGACTTTGCACATANGTCTCCAGCTCACAATAATGTAATTTGTTA	256	
Db	186	TGAGAACGACGACATGGATCTTTGCACACTATGCTTCCCAGCTCACAAAGTATCTGCTA	245	
Qy	257	CTTCCCCATGTAAT	270	
Db	246	CTTTCCCTGTTAAT	259	

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RESULT 11
US-10-006-252A-19
; Sequence 19, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Raphanus sativus
US-10-006-252A-19

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[illegible]

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Db      246 CTTTCCTTGTTAA 259

RESULT 12
US-09-732-561-13
; Sequence 13, Application US/09732561
; Patent No. US20020035739A1
; GENERAL INFORMATION:
; APPLICANT: Thomma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/01672
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; STRAIN: PDF 1.1
US-09-732-561-13

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Query Match	61.7%;	Score 176.6;	DB 9;	Length 403;
Best Local Similarity	83.5%;	Pred. No. 5e-47;		
Matches 213;	Conservative 0;	Mismatches 39;	Indels 3;	Gaps 1;
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Db	15	AAACAATAGTCAAGGCTAAGTCTGCTACCATCTGTACTCTTTTCTTCGCTGCTCTGTTT	74	
QY	79	TCCTTGTCTGCCCTTTGAAGCACCAACAATGGTGGATGCA--AGGTTGTGCGAGAGACCAA	135	
Db	75	TCCTTGTCTGCTCTTGAAGCACCGATGGTGGTGAACACAGAAGTTGTGCGAGAGCCAA	134	
QY	136	GTGGGACATGTCAGAGTTTCTGGGAACAACAATGCATGCAGGAACCAATGCAGAAACC	195	
Db	135	GTGGGACATGTCGCGAGTTTCGGGAACAGTAACCGGTGCAAGAAATCATGTCATTAAAC	194	
QY	196	TTGAAGAGCAGAACACCGATCTTGCAACTATGTCTTCCAGCTCACAATGTATTGTT	255	

Db 195 TTGAGAAACGACGATGGATCTTGCAACTATGCTCTTCCAGCTCACAAATGATCTGCT 254

QY 256 ACTTCCCATGTTAAT 270

Db 255 ACTTCCCATGTTAAT 269

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RESULT 13
US-09-732-561-15
? Sequence 15, Application US/09732561
? Patent No. US20020035738A1
? GENERAL INFORMATION:
? APPLICANT: Thomma, Bart
? APPLICANT: Terras, Franky
? APPLICANT: Penninckx, Iris
? APPLICANT: Manners, John
? APPLICANT: Kazan, Kemal
? APPLICANT: Broekaert, Willem
? TITLE OF INVENTION: Plant Protection Method
? NUMBER OF SEQUENCES: 24
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: ZENECA Ag Products
? STREET: 1800 Concord Pike
? CITY: Wilmington
? STATE: DE
? COUNTRY: USA

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/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB97/0167
/ FILING DATE: 20-JUN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Horenschutz, Liza D.
/ REGISTRATION NUMBER: 33,712
/ REFERENCE/DOCKET NUMBER: PPD 50161
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (302) 886-1699
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 400 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ ORIGINAL SOURCE:
/ STRAIN: PDF1.2
/
/ US-09-732-561-15

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QY	20	AGTAATAGATATGGCTAAAGTTTGGTACCATCATCTCTCTTCTCTTTTGGCTGCTCTGTGTCT	79		
Db	22	ATAATCATCATGGCTAAAGTTTGGTCTTCATCATCACCCCTTATCTTCGCTGCTCTGTGTCT	81		
QY	80	CTTTGCTGCTTTTGAAGCACCAACAATGGTGGATGCA---AGTTTGGCCAGACACCAAG	136		
Db	82	CTTTGCTGCTTTTCGACGCACCCGGCAATGGTGGANGACAGAGTTTGGCCAGACCAAG	141		
QY	137	TGGGACATGGTCAAGAGTTTGTGGGACACAACAAATGCATGCAGGAACCAATGCAGAAACCT	196		

Db 142 TGGACATGTCAGGGGTTTCGGAAACAGTAATGCATCAGAGAATCAGTCGATTAACT 201

QY 197 TGAAGAGCAGAAACAGGGATCTTGCAACTANGTCTTCCAGCTCACAAATGATTTGTTA 256

Db 202 TGAAGGAGCCAAACATGGATCATGCACATATGCTTCCAGCACAAAGTGATCTGTGA 261

QY 257 CTTCCCATGTTAA 269

Db 262 CGTCCCATGTTAA 274

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RESULT 14
US-09-887-576-607
; Sequence 607, Application US/09887576
; Patent No. US2002044047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 607
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(400)
; OTHER INFORMATION: n = A,T,C or G
US-09-887-576-607

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Query Match	61.6%;	Score 176.2;	DB 9;	Length 400;
Best Local Similarity	83.8%;	Pred. No. 6,7e-47;		
Matches 212; Conservative	0;	Mismatches 38;	Indels 3;	Gaps 1;
<hr/>				
QY	20	AGTAATAGATATGGCTAAAGTTTGCTACCATCATCTCTTCTCTTTGCTGCTCTGTGTCT	79	
Db	22	AATAATCATCATGGCTAAGTTTGCTTCATCATCACCCITATCTCGCTGCTGTGTCT	81	
<hr/>				
QY	80	CTTTGCTGCTTTGAAGCACCACCAATAGTGGTAGCA--AGTTGTGCAGAGACCAAG	136	
Db	82	CTTTGCTGCTTTGCAGCCACCGCAATGTTGGAAGCACAGAAGTTGTGCAGAAGCCAAG	141	
<hr/>				
QY	137	TGGGACATGCTCAGGAGTTTGTGGGAACAACATGTCATGCAGGAACCAATGCAGAACCT	196	
Db	142	TGGGACATGCTCAGGAGTTTGTGGGAACAACATGTCATGCAGGAACCAATGCAGAACCT	201	
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QY	197	TGAAAAGACAGAACACGGATCTTGCAACTATGTCCTCCAGCTCACAAATGATTGTGA	256	
Db	202	TGAAAGGCCAACATGGATCATGCAACTATGTCCTCCAGCAACAAGTGTATCTGTTA	261	
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QY	257	CTTCCCANGTTAA	269	
Db	262	CGTCCCATGTTAA	274	

RESULT 15  
US-09-759-584-58

; Sequence 58, Application US/09759584  
; Patent No. US20010014732A1  
; GENERAL INFORMATION:  
; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, FRANKY R.G.  
; APPLICANT: VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/759,584  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/377,687  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 43..282  
; US-09-759-584-58

Query Match 61.2%; Score 175; DB 9; Length 288;  
Best Local Similarity 83.1%; Pred.No.1.4e-46;  
Matches 212; Conservative 0; Mismatches 40; Indels 3; Gaps 1;  
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QY 93 TTTTGTGCTTTTGAAGACCAACAATGGTGGAGACCAAGTTGTGCCAAGGCCAAG 152  
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QY 137 TGGGACATGTCAGGAGTTTGGGAGCAACATGTCATGTCAGGAAACCATGCGAAACCT 196  
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QY 153 TGGGACATGTCAGGAGTTTGGGAGCAACATGTCATGTCAGGAAACCATGCGAAACCT 212  
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QY 213 TGAGAAAGCAGACATGATCTTGCACATATGCTTCCAGCTCACAATGATTTGTTA 272  
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QY 257 CTTCCCATGTTAATA 271  
Db |||||  
QY 273 CTTTCCCTGTTAATA 287  
Db |||||

Search completed: May 18, 2004, 20:33:21  
Job time : 264.25 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:05:11; Search time 2381.6 Seconds  
(without alignments)  
3586.070 Million cell updates/sec

Title: US-10-681-972-12

Perfect score: 286

Sequence: 1 99gaattcggtccaaagaaa.....taataaggatccgaattccc 286

Scoring table:

IDENTITY NUC

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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: em\_estmu:

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6: em\_estpl:

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8: em\_hcc:

9: gb\_est1:

10: gb\_est2:

11: gb\_hcc:

12: gb\_est3:

13: gb\_est4:

14: gb\_est5:

15: em\_estfun:

16: em\_estom:

17: em\_gss\_hum:

18: em\_gss\_inv:

19: em\_gss\_pln:

20: em\_gss\_vrt:

21: em\_gss\_fun:

22: em\_gss\_mam:

23: em\_gss\_mus:

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25: em\_gss\_rod:

26: em\_gss\_phg:

27: em\_gss\_vrt:

28: gb\_gss1:

29: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	177.8	62.2	447	14	CD832592

5	177.8	62.2	452	14	CD832071
6	177.8	62.2	458	14	CD834994
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9	176.6	61.7	422	9	AV787956
10	176.2	61.6	400	14	T04323
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12	176.2	61.6	409	14	CD834090
13	176.2	61.6	420	14	CD833944
14	176.2	61.6	421	14	CD826491
15	176.2	61.6	421	14	CD831111
16	176.2	61.6	421	14	CD833977
17	176.2	61.6	422	14	CD833983
18	176.2	61.6	426	14	CD827413
19	176.2	61.6	435	14	CD8259173
20	176.2	61.6	438	14	CD831479
21	176.2	61.6	450	14	CD834611
22	176.2	61.6	553	14	CD831014
23	175	61.2	403	14	Z27258
24	175	61.2	421	9	AV816118
25	175	61.2	422	9	AV788559
26	174.6	61.0	418	14	CD832625
27	174.6	61.0	419	14	CD834168
28	174.6	61.0	438	14	CD831294
29	174.6	61.0	453	14	CD834008
30	174.6	61.0	519	14	CD835064
31	173	60.5	421	14	CD837517
32	173	60.5	422	14	CD831972
33	173	60.5	424	14	CD833048
34	173	60.5	480	14	CD828332
35	169.2	59.2	473	14	CD834995
36	169.2	59.2	482	14	CD833627
37	167.8	58.7	345	13	BU238088
38	167.6	58.6	448	14	CD837588
39	167.6	58.6	476	14	CD833784
40	167.6	58.6	476	14	CD834092
41	167.6	58.6	481	14	CD833924
42	166	58.0	457	14	CD831226
43	166	58.0	457	14	CD831392
44	165	57.7	422	9	AV789144
45	164.6	57.6	421	9	AV789824

## ALIGNMENTS

RESULT 1  
BG321515  
LOCUS  
DEFINITION  
D801.08a06.R D801.AAFC ECORC cold stressed Flixweed seedlings  
Descurainia sophia cDNA clone D801\_08a06, mRNA sequence.  
410 bp mRNA linear EST 27-FEB-2001

ACCESSION  
BG321515  
GI:13151193

VERSION  
EST.

KEYWORDS  
SOURCE

ORGANISM

Descurainia sophia

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.

1 (bases 1 to 410)

Singh, J.A.; Piche, C.; Couroux, P.; De Moors, A.; Harris, L.J.;

Hattori, T.; Ouellet, T.; Robert, L.S.; Sprout, D. and Tinker, N.A.

Expressed Sequence Tags from Cold-Stressed Descurainia sophia

Seedlings

Unpublished (2001)

Contact: Singh, J.A.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-Food Canada

KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A

0C6, Canada

Tel: (613) 759-1662

Fax: (613) 759-1701

Email: singhja@em.agr.ca.



Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

#### FEATURES

source  
Location/Qualifiers  
1..446  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet neuf"  
/db\_xref="taxon:3708"  
/clone="BN45040H17"  
/tissue\_type="seed"  
/clone\_lib="BN45"

#### ORIGIN

Query Match 62.2%; Score 177.8; DB 14; Length 446;  
Best Local Similarity 84.2%; Pred. No. 6e-38; Mismatches 0; Indels 3; Gaps 1;  
Matches 213; Conservative 0; Mismatches 37; Indels 3; Gaps 1;  
QY 20 AGTAATAGATATGGCTAAAGTTTGTCTTACCATCATCTCTCTCTTTGTCTTTGTCTTTGTCT 79  
Db 56 ACTAGTGAGCATGGCTAAAGTTTGTCTTCCATCATTCGCCCACTTTTGTCTTTGTCTTTGTCT 115  
QY 80 CTTTGTCTGCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGGAGAGACCAAG 136  
Db 116 TTTTGTCTGCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGGAGAGACCAAG 175  
QY 137 TGGGACATGGTCAGGAGTTTGTGGAAACAACATGCGTGGAGACCAATGCGAAGACCT 196  
Db 176 TGGGACATGGTCAGGAGTTTGTGGAAACAACATGCGTGGAGACCAATGCGAAGACCT 235  
QY 197 TGAAGAGCAGCAACCGGATCTTCAACTATGTCTTCCAGCTCACAATATGTTTGTGA 256  
Db 236 TGAGAAAGCAGCAGATGGATCTTCAACTATGTCTTCCAGCTCACAAGTGTTTGTGA 295  
QY 257 CTTCCCATGTTAA 269  
Db 296 CTTCCCTTGTAA 308

RESULT 4  
CD832592  
LOCUS CD832592 447 bp mRNA linear EST 10-JUL-2003  
DEFINITION BN40.063015F011228 BN40 Brassica napus cDNA clone BN40063015, mRNA  
sequence.  
ACCESSION CD832592  
VERSION CD832592.1 GI:32514532  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

#### REFERENCE

1 (bases 1 to 447)  
Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

#### FEATURES

source  
Location/Qualifiers  
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/mol\_type="mRNA"  
/cultivar="Jet neuf"  
/db\_xref="taxon:3708"  
/clone="BN40063015"

/tissue\_type="seed"  
/clone\_lib="BN40"

#### ORIGIN

Query Match 62.2%; Score 177.8; DB 14; Length 447;  
Best Local Similarity 84.2%; Pred. No. 6e-38; Mismatches 0; Indels 3; Gaps 1;  
Matches 213; Conservative 0; Mismatches 37; Indels 3; Gaps 1;  
QY 20 AGTAATAGATATGGCTAAAGTTTGTCTTACCATCATCTCTCTTTGTCTTTGTCTTTGTCT 79  
Db 55 ACTAGTGAGCATGGCTAAAGTTTGTCTTCCATCATTCGCCCACTTTTGTCTTTGTCTTTGTCT 114  
QY 80 CTTTGTCTGCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGGAGAGACCAAG 136  
Db 115 TTTTGTCTGCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGGAGAGACCAAG 174  
QY 137 TGGGACATGGTCAGGAGTTTGTGGAAACAACATGCGTGGAGACCAATGCGAAGACCT 196  
Db 175 TGGGACATGGTCAGGAGTTTGTGGAAACAACATGCGTGGAGACCAATGCGAAGACCT 234  
QY 197 TGAAGAGCAGCAACCGGATCTTCAACTATGTCTTCCAGCTCACAATATGTTTGTGA 256  
Db 235 TGAGAAAGCAGCAGATGGATCTTCAACTATGTCTTCCAGCTCACAAGTGTTTGTGA 294  
QY 257 CTTCCCATGTTAA 269  
Db 295 CTTCCCTTGTAA 307

#### RESULT 5

CD832071 452 bp mRNA linear EST 10-JUL-2003  
LOCUS CD832071  
DEFINITION BN40.061003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA  
sequence.  
ACCESSION CD832071  
VERSION CD832071.1 GI:32514011  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

#### REFERENCE

1 (bases 1 to 452)  
Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

#### FEATURES

source  
Location/Qualifiers  
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/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet neuf"  
/db\_xref="taxon:3708"  
/clone="BN40061003"  
/tissue\_type="seed"  
/clone\_lib="BN40"

#### ORIGIN

Query Match 62.2%; Score 177.8; DB 14; Length 452;  
Best Local Similarity 84.2%; Pred. No. 6e-38; Mismatches 0; Indels 3; Gaps 1;  
Matches 213; Conservative 0; Mismatches 37; Indels 3; Gaps 1;  
QY 20 AGTAATAGATATGGCTAAAGTTTGTCTTACCATCATCTCTCTTTGTCTTTGTCTTTGTCT 79  
Db 60 ACTAGTGAGCATGGCTAAAGTTTGTCTTCCATCATTCGCCCACTTTTGTCTTTGTCTTTGTCT 119

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QY 80 CTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCA---AGTTGTGGAGAGACCAAG 136
Db 120 TTTTCGCTGCTTTGAGAGCACCACCAATGGTGGAGACCAAGTTGTGGAGAGGCGAAG 179
QY 137 TGGGACATGCTCAGGAGTTTGTGGGACCAACAAATGATGAGGAGCAATGAGAAACCT 196
Db 180 TGGGACATGCTCAGGAGTTTGTGGGACCAACAAATGATGAGGAGCAATGAGAAACCT 239
QY 197 TGAAGAGACGACGACGATCTTGGCACTATGCTTCCAGCTCAAAATGATTTGTTA 256
Db 240 TGAGAAAGCAGCAGATGATCTTGGCACTATGCTTCCAGCTCAAAATGATTTGTTA 299
QY 257 CTTCCCATGTTAA 269
Db 300 CTTCCCTTGTAA 312

RESULT 6
CD834994
LOCUS
DEFINITION
CD834994 458 bp mRNA linear EST 10-JUL-2003
Brassica napus cdna clone BN45043006, mRNA
ACCESSION
CD834994
VERSION
CD834994.1 GI:32516934
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 458)
AUTHORS
Genoplante.
TITLE
Genoplante, a major partnership french program in plant genomics
JOURNAL
Unpublished (2003)
COMMENT
Contact: Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
location=Brassica napus
mol_type=mRNA
cultivar=Jett neuf
db_xref=taxon:3708
clone=BN45043006
tissue_type=seed
clone_lib=BN45

FEATURES
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/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jett neuf"
/db_xref="taxon:3708"
/clone="BN45043006"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match 62.2%; Score 177.8; DB 14; Length 458;
Best Local Similarity 84.2%; Pred. No. 6e-38;
Matches 213; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 20 AGTAATAGATATGGCTAAGTTTGTCCATCATCTCTCTCTTGTGCTGCTTTCTTCT 79
Db 56 ACTAGTGAGCATGGCTAAGTTTGTCCATCATCTCTCTCTTGTGCTGCTTTCTTCTTCT 115
QY 80 CTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCA---AGTTGTGGAGAGACCAAG 136
Db 116 TTTTCGCTGCTTTGAGGACCAACCAATGGTGGAGACCAAGTTGTGGAGAGGCGCAAG 175
QY 137 TGGGACATGCTCAGGAGTTTGTGGGACCAACAAATGATGAGGAGCAATGAGAAACCT 196
Db 176 TGGGACATGCTCAGGAGTTTGTGGGACCAACAAATGATGAGGAGCAATGAGAAACCT 235
QY 197 TGAAGAGACGACGACGATCTTGGCACTATGCTTCCAGCTCAAAATGATTTGTTA 256
Db 236 TGAGAAAGCAGCAGATGATCTTGGCACTATGCTTCCAGCTCAAAATGATTTGTTA 295

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QY 257 CTTCCCATGTTAA 269
Db 296 CTTCCCTTGTAA 308

RESULT 7
CD831680
LOCUS
DEFINITION
CD831680 470 bp mRNA linear EST 10-JUL-2003
Brassica napus cdna clone BN40060H13, mRNA
ACCESSION
CD831680
VERSION
CD831680.1 GI:32513620
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 470)
AUTHORS
Genoplante.
TITLE
Genoplante, a major partnership french program in plant genomics
JOURNAL
Unpublished (2003)
COMMENT
Contact: Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
location=Brassica napus
mol_type=mRNA
cultivar=Jett neuf
db_xref=taxon:3708
clone=BN40060H13
tissue_type=seed
clone_lib=BN40

FEATURES
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/mol_type="mRNA"
/cultivar="Jett neuf"
/db_xref="taxon:3708"
/clone="BN40060H13"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Query Match 62.2%; Score 177.8; DB 14; Length 470;
Best Local Similarity 84.2%; Pred. No. 6e-38;
Matches 213; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 20 AGTAATAGATATGGCTAAGTTTGTCCATCATCTCTCTCTTGTGCTGCTTTCTTCTTCT 79
Db 78 ACTAGTGAGCATGGCTAAGTTTGTCCATCATCTCTCTCTTGTGCTGCTTTCTTCTTCT 137
QY 80 CTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCA---AGTTGTGGAGAGACCAAG 136
Db 138 TTTTCGCTGCTTTGAGGACCAACCAATGGTGGAGACCAAGTTGTGGAGAGGCGCAAG 197
QY 137 TGGGACATGCTCAGGAGTTTGTGGGACCAACAAATGATGAGGAGCAATGAGAAACCT 196
Db 198 TGGGACATGCTCAGGAGTTTGTGGGACCAACAAATGATGAGGAGCAATGAGAAACCT 257
QY 197 TGAAGAGACGACGACGATCTTGGCACTATGCTTCCAGCTCAAAATGATTTGTTA 256
Db 258 TGAGAAAGCAGCAGATGATCTTGGCACTATGCTTCCAGCTCAAAATGATTTGTTA 317
QY 257 CTTCCCATGTTAA 269
Db 318 CTTCCCTTGTAA 330

RESULT 8
BG321454
LOCUS
DEFINITION
BG321454 394 bp mRNA linear EST 27-FEB-2001
Dsol_08h05_A Dsol_AAFc_ECORC_cold stressed Flaxweed seedlings
Descurainia sophia cdna clone Dsol_08h05, mRNA sequence.
ACCESSION
BG321454
VERSION
BG321454.1 GI:13151132

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 422)

Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.

Large scale analysis of Arabidopsis full-length cDNA (2002b)

Unpublished (2002)

Contact: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: mseki@tc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pluscript vector as a SstI/XhoI insert. Please visit our web site (<http://www.gsc.riken.go.jp/e/plant/index.e.html>) for

FEATURES	source
further details.	Location/Qualifiers
	1. .422
	/organism="Arabidopsis thaliana"
	/mol_type="mRNA"
	/db_xref="taxon:3702"
	/clone="RAFL06-77-K06"
	/dev_stage="plants at various developmental stages from germination to mature seeds"
	/lab_host="DH10B"
	/clone_lib="RAFL6"
	/note="Site 1: SsII; Site 2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) treatments"

	Query Match	61.7%;	Score 176.6;	DB 9;	Length 422;
	Best Local Similarity	83.5%;	Pred. No. 1.3e-37;		
	Matches 213;	Conservative 0;	Mismatches 39;	Indels 3;	Gaps 1;
QY	19	RAGTAATAGATATGCTAAGTTTGCTACATCATCTCTTCTCTTTGGTCGTCTTTGTTTC	78		
Db	332	AAACAATAATGTCATGGCTAAGTCTGTGCATCGTTACTCTTTCTCTGGTCGTCTTTGTTT	333		
QY	79	TCTTTGGCTGCCCTTTGAAGCACCAACAATGGTGGATGCA--AGETTTGCGAGAGACCAA	135		
Db	332	TCTTTGGCTGCTTTGAAGCACCAGTGGTGGGAAGCACAGAAGTTGTCCGAGAGCCNA	273		
QY	136	GTGGGACATGTCAGGAGTTTTGTGGAAACAACATGCA TGCAGGACCAATGCAGAAACC	195		
Db	272	GTGGGACATGTCGGAGTTTTCGGGAAACAGTAACGGCTGCAAGAATCAGTGCATTAAACC	213		
QY	196	TTGAAAGACGAGAACACGGATCTTTCGCACTATGCTTCCCAGCTCACAAAATGTTATTTGT	255		
Db	212	TTGAGAAGACGACATGSAATCTTTCGAATATGCTTCCCAGCTCACAAATGTTATCTGCT	153		
QY	256	ACTTCCCATGTTTAAT	270		
Db	152	ACTTCCCATGTTTAAT	138		

RESULT 10	
T04323	
LOCUS	400 bp
DEFINITION	370 Lambda-PRL2 Arabidopsis thaliana CDNA clone 37F10T7, mRNA
ACCESSION	T04323
VERSION	T04323.1
KEYWORDS	EST.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana

Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

## FEATURES

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1. 409
    /organism="Brassica napus"
    /mol_type="mRNA"
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    /db_xref="taxon:3708"
    /clone="BN45040121"
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    /cissue_lib="BN45"
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## ORIGIN

Query Match	61.6%;	Score 176.2;	DB 14;	Length 409;
Best Local Similarity	83.8%;	Pred. No. 1.6e-37;		
Matches 212:	Conservative	0;	Mismatches 38;	Indels 3;
				Gaps 1;

QY  
20 AGTAAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTTCTCTTTGCTGCCTCCTGCTTCCT 75  
20 TACTCTGCT 78

80 CTTTGCTGCTTTGAAGACCAACAATGGTGGATGCA--AGTTTGTGGAGAGACCAAG 136

QY 137 TGGACATGGTCTCAGGAGTTTGTGGGAAACAACAATGCGATGCGGAAACCAATGCGAAACCT 196

197 TGAAGAGCGAACAACGGATCTTGGCAACTATGTCTTCCAGCTCACAAAATGTTTGTTA 256

DB  
199 TGAAGGACCGCAGCACTGGTCTTTCTG  
QY 257 CTTCCCATGTAA 269  
          |||||

Db 259 CTTCCCTGTTAA 2/1

[illegible]

ACCESSION	VERSION	GI
CD833944	CD833944.1	32515884

SOURCE	ORGANISM
Brassica napus (rape)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Brassica napus
Brassica napus	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Brassica napus

rosids; euforids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 420)

REFERENCE

ATHYRUS

ATHYRUS

Genoplante.

Unpublished (2003)  
Contact: Genoplate

93, rue Henri Rochefort 91043 Evry  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10

**FEATURES**  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)  
and <http://genoplante-info.infobiogen.fr>.  
Location/Qualifiers

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/organism="Brassica napus"
/mol type="mRNA"
/mol fixax="Tet nalf"

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/dev_xfs1= LEXON:3700
/clone="BN45040B07"
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## ORIGIN

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Query Match      61.6%;   Score 176.2;   DB 14;   Length 420;
Best Local Similarity 83.8%;
Pred. No. 1.6e-37;
Matches 212; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

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20 AGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTTCTTCTTGTGCGCTCTTGTCCT

99

80 CTTTGGTGCCTTTGAAGACCAACAAATGGTGGATGCA---AGTTGTGTGCAGAGACCAAG 136

137 TGGGACATGGTCAGGAGTTTGTGGGAACACAAATGCATGCAGGGAACCAATGCAGAAACCT 196

197 TGAAGAGCAGGAACACGGATCTTGGAACTATGCTCTCCAGCTCAGAAATGATTGTGA 256

DB  
Z20 TGAAGGACCACTTCCATTTTCATT  
QY 257 CTTCCCATGTAA 269  
TTTTTT

Db  
280 CTTCCTTGTTAA 292

	CD826491	LOCUS	EST 10-JUL-2000
	421 bp	mRNA	linear
	BN25	Brassica napus cDNA clone BN25064A05,	mRNA

Accession	Version	Sequence
CD826491	GI:32508431	

SOURCE	Brassica napus (rape)
ORGANISM	Brassica napus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

Genopiantes  
Unpublished (2003)  
Contact: Genopiantes  
Genopiantes

93, rue henri rocheport 91000 evry  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10

**FEATURES**  
Location/Qualifiers  
and <http://genoplante-info.inbioogen.fr>.  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)

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source
/organism="Brassica napus"
/mol_type="mRNA"
/submitter="JGI"

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/wd_xref= taxon:3700
/clone="BN25064A05"
/tissue_type="seed"
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	61.6%	176.2	14	421

Matches 212; Conservative 0; Mismatches 38; Indels 3; Gaps 2

Db  
41 ACTAGTGATCATGGCTAAGTTTGCTCCATCATGGCCTACITTTTGGTGTCTCTGTGCTT



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 16:14:01 ; Search time 757.05 Seconds  
(without alignments)  
8616.891 Million cell updates/sec

Title: US-10-681-972-12\_COPY\_116\_269  
Perfect score: 154  
Sequence: 1 aaggttgaggagagacaa.....ttgttacttcccatgtaa 154

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

##### GenEmbl.\*

1: gb ba.\*  
2: gb htg.\*  
3: gb in.\*  
4: gb om.\*  
5: gb ov.\*  
6: gb pat.\*  
7: gb ph.\*  
8: gb pl.\*  
9: gb pr.\*  
10: gb ro.\*  
11: gb sts.\*  
12: gb sy.\*  
13: gb un.\*  
14: gb vi.\*  
15: em ba.\*  
16: em fun.\*  
17: em hum.\*  
18: em in.\*  
19: em mu.\*  
20: em om.\*  
21: em or.\*  
22: em ov.\*  
23: em pat.\*  
24: em ph.\*  
25: em pl.\*  
26: em ro.\*  
27: em sts.\*  
28: em un.\*  
29: em vi.\*  
30: em htg\_hum.\*  
31: em htg\_inv.\*  
32: em htg\_other.\*  
33: em htg\_mus.\*  
34: em htg\_pln.\*  
35: em htg\_rod.\*  
36: em htg\_mam.\*  
37: em htg\_vrt.\*  
38: em sy.\*  
39: em htgo\_hum.\*  
40: em htgo\_mus.\*  
41: em htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	154	100.0	270	6	AR014691 Sequence
2	154	100.0	270	6	AR432391 Sequence
3	154	100.0	286	6	AR014689 Sequence
4	154	100.0	286	6	AR432389 Sequence
5	140.2	91.0	500	6	AR014686 Sequence
6	140.2	91.0	500	6	AR432386 Sequence
7	122.6	79.6	526	11	BV010709
8	122.6	79.6	574	11	BV010696
9	122.6	79.6	575	11	BV010710
10	122.6	79.6	578	11	BV010700
11	122.6	79.6	602	11	BV010703
12	122.6	79.6	61290	8	AB017065
13	122.6	79.6	87080	8	AC004747
14	121	78.6	580	11	BV010699
15	121	78.6	582	11	BV010698
16	121	78.6	595	11	BV010707
17	121	78.6	604	11	BV010711
18	119.4	77.5	243	6	AX412406
19	119.4	77.5	243	6	AX412601
20	119.4	77.5	243	6	AX651878
21	119.4	77.5	243	8	AY060506
22	119.4	77.5	403	6	A68645
23	119.4	77.5	403	8	ATANTSPEC
24	119.4	77.5	425	8	AY052236
25	119.4	77.5	497	11	BV010712
26	119.4	77.5	541	11	BV010697
27	119.4	77.5	563	11	BV010667
28	119.4	77.5	572	11	BV010673
29	119.4	77.5	578	11	BV010671
30	119.4	77.5	579	11	BV010670
31	119.4	77.5	95870	8	AC007396
32	117.8	76.5	243	6	AX412329
33	117.8	76.5	243	6	AX412502
34	117.8	76.5	243	6	AX507351
35	117.8	76.5	243	6	AX590057
36	117.8	76.5	243	6	BD174927
37	117.8	76.5	274	8	AY133787
38	117.8	76.5	395	8	RSU18557
39	117.8	76.5	400	6	A68647
40	117.8	76.5	414	6	A26875
41	117.8	76.5	414	6	A39549
42	117.8	76.5	414	6	A63404
43	117.8	76.5	414	6	AR050153
44	117.8	76.5	414	6	AR130272
45	117.8	76.5	414	6	E31545

#### ALIGNMENTS

RESULT 1  
AR014691  
LOCUS AR014691 270 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 14 from patent US 5773696.  
ACCESSION AR014691  
VERSION AR014691.1 GI:3972145  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 270)  
AUTHORS Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.  
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi  
JOURNAL Patent: US 5773696-A 14 30-JUN-1998;

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FEATURES             Location/Qualifiers
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                        /organism="unknown"
                        /mol_type="unassigned DNA"
ORIGIN
Query Match          100.0%; Score 154; DB 6; Length 270;
Best Local Similarity 100.0%; Pred. No. 3.8e-36;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 60
    |||
Db 108 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACGGATCTTGCACACTATGTCTTCCC 120
    |||
Db 168 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACGGATCTTGCACACTATGTCTTCCC 227
QY 121 AGCTCACAATGTATTGTGTACTTCCCATGTTAA 154
    |||
Db 228 AGCTCACAATGTATTGTGTACTTCCCATGTTAA 261

RESULT 2
LOCUS               AR432391                270 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION          Sequence 14 from patent US 6653280.
ACCESSION            AR432391
VERSION              AR432391.1 GI:40194668
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 270)
AUTHORS              Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE               Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 14 25-NOV-2003;
JOURNAL              Location/Qualifiers
FEATURES             1..270
   source            /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN
Query Match          100.0%; Score 154; DB 6; Length 270;
Best Local Similarity 100.0%; Pred. No. 3.8e-36;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 60
    |||
Db 108 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACGGATCTTGCACACTATGTCTTCCC 120
    |||
Db 168 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACGGATCTTGCACACTATGTCTTCCC 227
QY 121 AGCTCACAATGTATTGTGTACTTCCCATGTTAA 154
    |||
Db 228 AGCTCACAATGTATTGTGTACTTCCCATGTTAA 261

RESULT 3
LOCUS               AR014689                286 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION          Sequence 12 from patent US 5773696.
ACCESSION            AR014689
VERSION              AR014689.1 GI:3972143
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 286)
AUTHORS              Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.

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TITLE               Antifungal polypeptide and methods for controlling plant pathogenic
fungi
JOURNAL              Patent: US 5773696-A 12 30-JUN-1998;
FEATURES             Location/Qualifiers
   source            1..286
                        /organism="unknown"
                        /mol_type="unassigned DNA"
ORIGIN
Query Match          100.0%; Score 154; DB 6; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.8e-36;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 60
    |||
Db 116 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 175
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACGGATCTTGCACACTATGTCTTCCC 120
    |||
Db 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACGGATCTTGCACACTATGTCTTCCC 235
QY 121 AGCTCACAATGTATTGTGTACTTCCCATGTTAA 154
    |||
Db 236 AGCTCACAATGTATTGTGTACTTCCCATGTTAA 269

RESULT 4
LOCUS               AR432389                286 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION          Sequence 12 from patent US 6653280.
ACCESSION            AR432389
VERSION              AR432389.1 GI:40194666
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 286)
AUTHORS              Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE               Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 12 25-NOV-2003;
JOURNAL              Location/Qualifiers
FEATURES             1..286
   source            /organism="unknown"
                        /mol_type="genomic DNA"
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Query Match          100.0%; Score 154; DB 6; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.8e-36;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 60
    |||
Db 116 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 175
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACGGATCTTGCACACTATGTCTTCCC 120
    |||
Db 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACGGATCTTGCACACTATGTCTTCCC 235
QY 121 AGCTCACAATGTATTGTGTACTTCCCATGTTAA 154
    |||
Db 236 AGCTCACAATGTATTGTGTACTTCCCATGTTAA 269

RESULT 5
LOCUS               AR014686                500 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION          Sequence 9 from patent US 5773696.
ACCESSION            AR014686
VERSION              AR014686.1 GI:3972140
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM             Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 500)
AUTHORS Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic
JOURNAL fungi
FEATURES Patent: US 5773696-A 9 30-JUN-1998;
source Location/Qualifiers
1..500
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 91.0%; Score 140.2; DB 6; Length 500;
Best Local Similarity 94.8%; Pred.No.6.1e-32;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGGTTGTCGAGAGACCAAGTGGACATGTCAGAGTTTGGGAACAACATGATGC 61
Db |||||||
159 AAGTTGTCGAGAGTCCAGTGGAAATGTCAGCGGTGTGGGAATAATAACGATGC 218
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 121
Db |||||||
219 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 278
QY 122 GCTCACAATGTTATTTGTTACTTCCCATGTTAA 154
Db |||||||
279 GCTCACAATGTTATTTGTTACTTCCCATGTTAA 311

RESULT 6
LOCUS AR432386 500 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6653280.
ACCESSION AR432386
VERSION AR432386.1 GI:40194663
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 500)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide AlyAFP from Alysum and methods for
controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 9 25-NOV-2003;
FEATURES Location/Qualifiers
1..500
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 91.0%; Score 140.2; DB 6; Length 500;
Best Local Similarity 94.8%; Pred.No.6.1e-32;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGGTTGTCGAGAGACCAAGTGGACATGTCAGAGTTTGGGAACAACATGATGC 61
Db |||||||
159 AAGTTGTCGAGAGTCCAGTGGAAATGTCAGCGGTGTGGGAATAATAACGATGC 218
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 121
Db |||||||
219 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 278
QY 122 GCTCACAATGTTATTTGTTACTTCCCATGTTAA 154
Db |||||||
279 GCTCACAATGTTATTTGTTACTTCCCATGTTAA 311

RESULT 7
BV010709 526 bp DNA linear STS 18-JUL-2003
LOCUS MASC STS16442 Arabidopsis thaliana (Landsberg erecta accession)
DEFINITION Genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
ACCESSION BV010709

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VERSION BV010709.1 GI:32963207
KEYWORDS STS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 526)
AUTHORS Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitcheil-Olds,T. and Weisshaar,B.
TITLE Large-Scale Identification and Analysis of Genome-Wide
JOURNAL Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
MEDLINE Genome Res. 13 (6), 1250-1257 (2003)
PUBMED 22683290
COMMENT Synonyms: PCP16C2 ler.a
Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571465
Fax: + 49-3641-571402
Email: schmid@ice.mpg.de
Primer A: CGCTGCTCTGTTCTCTTTG
Primer B: AAACAAACCGTTGTTGGTCA
STS size: 526
PCR Profile:
  Presoak: 94 degrees for 2.00 minute(s)
  Denaturation: 94 degrees for 0.50 minute(s)
  Annealing: 58 degrees for 0.50 minute(s)
  Polymerization: 72 degrees for 1.00 minute(s)
  PCR Cycles: 35
  Thermal Cycler: Perkin Elmer GeneAmp9600
  Protocol:
    Template: 20 - 100 ng
    Primer: each 1 uM
    dNTPs: each 400 uM
    Taq Polymerase: 0.05 units/uL
    Total Vol: 10 uL
  Buffer:
    MgCl2: 1.5 mM
    KCl: 50 mM
    Tris-HCl: 10 mM
    pH: 8.3.
  FEATURES
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        /organism="Arabidopsis thaliana"
        /mol_type="genomic DNA"
        /strain="Landsberg erecta"
        /db_xref="taxon:3702"
        /clone_lib="Arabidopsis thaliana (Landsberg erecta
        accession) genomic DNA"
        /notes="Genomic DNA prepared from rosette leaves. DNA was
        amplified and directly sequenced from both directions and
        assembled into a consensus sequence. Note: Sequencing
        granted in the context of the GABI Arabidopsis Verbund:
        Genetic Diversity, 'Establishment of high-efficiency
        SNP-based mapping tools and development of methods for
        genome-wide mutation detection' PIs: Thomas Altmann,
        Thomas Mitchell-Olds, Bernd Weisshaar"
        <1..>526
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ORIGIN
Query Match 79.6%; Score 122.6; DB 11; Length 526;
Best Local Similarity 87.6%; Pred.No.1.4e-26;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTTCTGCGAGACCAAGTGGACATGTCAGAGTTTGGGAACAACATGATGC 61
Db |||||||
42 AAGTTTCTGCGAGAACCAAGTGGTACTTGTTCAGAGTTTGGGAACAACATGATGC 101
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 121

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Db 102 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGATCTTGCACACTATGTCTTCCCA 161  
 QY 122 GCTCACAAATGTTTCTTACTTCCCATGTAA 154  
 Db 162 GCTCACAAAGTATCTTCTTACCTGCTCCCATGTAA 194

RESULT 8  
 BV010696/c 574 bp DNA linear STS 18-JUL-2003  
 LOCUS MASC\_STS16441 Arabidopsis thaliana (Eifel-2 accession) genomic DNA  
 DEFINITION Arabidopsis thaliana STS genomic, sequence tagged site.

ACCESSION BV010696  
 VERSION BV010696.1 GI:32963194  
 KEYWORDS STS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 574)

AUTHORS Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,

Mitchell-Olds,T. and Weisshaar,B.

Large-Scale Identification and Analysis of Genome-Wide

Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana

Genome Res. 13 (6), 1250-1257 (2003)

22683290

PUBMED 12799357

COMMENT Synonyms: PCP16C2.ei2.a

Contact: Karl Schmid

Department of Genetics and Evolution

Max-Planck-Institute of Chemical Ecology

Winzerlaer Str. 10, 07745 Jena, Germany

Tel: + 49-3641-571465

Fax: + 49-3641-571402

Email: schmid@ice.mpg.de

Primer A: CGCTGCTCTTGTCTCTTTTG

Primer B: AAACAACCGTTGTGTGTC

STS size: 574

PCR Profile:

Presoak: 94 degrees for 2.00 minute(s)

Denaturation: 94 degrees for 0.50 minute(s)

Annealing: 58 degrees for 0.50 minute(s)

Polymerization: 72 degrees for 1.00 minute(s)

PCR Cycles: 35

Thermal Cycler: Perkin Elmer GeneAmp9600

Protocol:

Template: 20 - 100 ng

Primer: each 1 uM

dNTPs: each 400 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 8.3.

Location/Qualifiers

1..574

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Eifel-2"

/db\_xref="taxon:3702"

/clone\_lib="Arabidopsis thaliana (Bifel-2 accession)

genomic DNA"

/note="Genomic DNA prepared from rosette leaves. DNA was

amplified and directly sequenced from both directions and

assembled into a consensus sequence. Note: Sequencing

granted in the context of the GABI Arabidopsis Verbund:

Genetic Diversity, 'Establishment of high-efficiency

SNP-based mapping tools and development of methods for

genome-wide mutation detection' Pls: Thomas Altmann,  
 Thomas Mitchell-Olds, Bernd Weisshaar"  
 <1..574

STS  
 ORIGIN

Query Match 79.6%; Score 122.6; DB 11; Length 574;

Best Local Similarity 87.6%; Pred. No. 1.4e-26;

Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGGAGAGACAAAGTGGACATGTCAGGAGTTTGTGGGAACCAACAATGCATGC 61

Db 486 AAGTTGTGGAGAGACAAAGTGGTACTTGTGTAGGAGTTTGTGGGAACCAACAATGCATGC 427

QY 62 AGAACCAATGACGAACCTTGAAGAGACAGACAGGATCTTGGCACTATGTCCTCCCA 121

Db 426 AAGAATCAGTGCATTAACCTTGAAGAGACAAACATGGATCTTGGCACTATGTCCTCCCA 367

QY 122 GCTCACAAATGTTTGTGTACTTCCCATGTAA 154

Db 366 GCTCACAAAGTATCTGTTACGTCCTCCCATGTAA 334

RESULT 9

BV010710

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

Arabisopsis thaliana (thale cress)

Arabisopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 575)

AUTHORS Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,

Mitchell-Olds,T. and Weisshaar,B.

Large-Scale Identification and Analysis of Genome-Wide

Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana

Genome Res. 13 (6), 1250-1257 (2003)

22683290

PUBMED 12799357

COMMENT Synonyms: PCP16C2.wei0.a

Contact: Karl Schmid

Department of Genetics and Evolution

Max-Planck-Institute of Chemical Ecology

Winzerlaer Str. 10, 07745 Jena, Germany

Tel: + 49-3641-571465

Fax: + 49-3641-571402

Email: schmid@ice.mpg.de

Primer A: CGCTGCTCTTGTCTCTTTTG

Primer B: AAACAACCGTTGTGTGTC

STS size: 575

PCR Profile:

Presoak: 94 degrees for 2.00 minute(s)

Denaturation: 94 degrees for 0.50 minute(s)

Annealing: 58 degrees for 0.50 minute(s)

Polymerization: 72 degrees for 1.00 minute(s)

PCR Cycles: 35

Thermal Cycler: Perkin Elmer GeneAmp9600

Protocol:

Template: 20 - 100 ng

Primer: each 1 uM

dNTPs: each 400 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 8.3.

Location/Qualifiers

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/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Eifel-2"

/db\_xref="taxon:3702"

/clone\_lib="Arabidopsis thaliana (Bifel-2 accession)

genomic DNA"

/note="Genomic DNA prepared from rosette leaves. DNA was

amplified and directly sequenced from both directions and

assembled into a consensus sequence. Note: Sequencing

granted in the context of the GABI Arabidopsis Verbund:

Genetic Diversity, 'Establishment of high-efficiency

SNP-based mapping tools and development of methods for



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FEATURES
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  Location/Qualifiers
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      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
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      /db_xref="taxon:3702"
      /clone_lib="Arabidopsis thaliana (Weininger-0 accession)"
      /notes="Genomic DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and assembled into a consensus sequence. Note: Sequencing granted in the context of the GABI Arabidopsis Verbund: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PIs: Thomas Altmann, Thomas Mitchell-Olds, Bernd Weisshaar"
      <1..575

STSS
ORIGIN
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  Best Local Similarity 87.6%; Pred. No. 1.4e-26;
  Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGACATGTCAGGAGTTGTGGGAACAATGCATGC 61
    |||||
Db   92 AAGTTGTGCGAGAGACCAAGTGGTACTGTCAGGAGTTGTGGGAACAATGCATGC 151
    |||||
QY  62 AGGAACCAATGCAGAACCTTGAAGAGCAGACACGATCTTGCACACTATGCTTCCCA 121
    |||||
Db   152 AAGAATCAGTGCAATTAACCTTGAAGAGCAGACACGATCTTGCACACTATGCTTCCCA 211
    |||||
QY  122 GCTCACAAATGATTTGTTACTTCCCATGTTAA 154
    |||||
Db   212 GCTCACAAAGTATCTGTTAGTCCCATGTTAA 244
    |||||

RESULT 10
BV010700/c
LOCUS
DEFINITION
  MASC STS16437 Arabidopsis thaliana (Lezoux/Puy-de-Dome-0 accession)
  genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
VERSION
  BV010700.1 GI:32963198
KEYWORDS
  STS.
SOURCE
  Arabidopsis thaliana (thale cress)
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
  1 (bases 1 to 578)
  Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
  Mitchell-Olds,T. and Weisshaar,B.
  Large-Scale Identification and Analysis of Genome-Wide
  Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
  Genome Res. 13 (6), 1250-1257 (2003)
  22683290
  PUBMED
COMMENT
  Synonyms: PCP16C2.1z0.a
  Department of Genetics and Evolution
  Max-Planck-Institute of Chemical Ecology
  Winzlerlaer Str. 10, 07745 Jena, Germany
  Tel: + 49-3641-571465
  Fax: + 49-3641-571402
  Email: schmid@ice.mpg.de
  Primer A: CGCTGCTCTGTCTCTCTTTG
  Primer B: AAACAACCGTGTGTGGTCA
  STS size: 578
  PCR Profile:
    Presoak: 94 degrees for 2.00 minute(s)
    Denaturation: 94 degrees for 0.50 minute(s)
    Annealing: 58 degrees for 0.50 minute(s)
    Polymerization: 72 degrees for 1.00 minute(s)

FEATURES
source
  Location/Qualifiers
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      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
      /strain="Lezoux/Puy-de-Dome-0"
      /db_xref="taxon:3702"
      /clone_lib="Arabidopsis thaliana (Lezoux/Puy-de-Dome-0 accession)"
      /notes="Genomic DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and assembled into a consensus sequence. Note: Sequencing granted in the context of the GABI Arabidopsis Verbund: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PIs: Thomas Altmann, Thomas Mitchell-Olds, Bernd Weisshaar"
      <1..578

STSS
ORIGIN
  Query Match      79.6%; Score 122.6; DB 11; Length 578;
  Best Local Similarity 87.6%; Pred. No. 1.4e-26;
  Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGACATGTCAGGAGTTGTGGGAACAATGCATGC 61
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Db   486 AAGTTGTGCGAGAGACCAAGTGGTACTGTCAGGAGTTGTGGGAACAATGCATGC 427
    |||||
QY  62 AGGAACCAATGCAGAACCTTGAAGAGCAGACACGATCTTGCACACTATGCTTCCCA 121
    |||||
Db   426 AAGAATCAGTGCAATTAACCTTGAAGAGCAGACACGATCTTGCACACTATGCTTCCCA 367
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QY  122 GCTCACAAATGATTTGTTACTTCCCATGTTAA 154
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Db   366 GCTCACAAAGTATCTGTTAGTCCCATGTTAA 334
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RESULT 11
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DEFINITION
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VERSION
  BV010703
KEYWORDS
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SOURCE
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  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
  1 (bases 1 to 602)
  Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
  Mitchell-Olds,T. and Weisshaar,B.
  Large-Scale Identification and Analysis of Genome-Wide
  Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
  Genome Res. 13 (6), 1250-1257 (2003)
  22683290
  PUBMED
COMMENT
  Synonyms: PCP16C2.gue0.a
  Contact: Karl Schmid

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CDS

CDS

CDS

CDS

Query Match

Best Local Similarity 79.6%; Score 122.6; DB 8; Length 61290;  
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 2 AGGTTGTCGAGACCAAGTGGGACATGGTCAGAGTTTGGGAAACAAATGCATGC 61  
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Qy 62 AGGAACCAATCAGAAACCTTGAAGAGACGACACACGATCTTGCAACTATGTCTTCCCA 121  
Db 22629 AAGATCAGTCATTAACCTTGAGGGAGCAAAACATGGATCTTGCACACTATGTCTTCCCA 22570

Qy 122 GCTCACAATATGATTGTACTTCCCAATGTTAA 154

Db 22569 GCTCACAATATGATTGTACTTCCCAATGTTAA 22537

RESULT 13

AC004747/c

LOCUS

DEFINITION

AC004747

Arabisopsis thaliana chromosome 2 clone T19L18 map B68, complete

sequence.

AC004747

VERSION

AC004747.3

KEYWORDS

HTG.

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/note="contains similarity to UDP-glucose 4-epimerase

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79.6%; Score 122.6; DB 8; Length 61290;

Best Local Similarity 87.6%; Pred. No. 1.4e-26;

Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 2 AGGTTGTCGAGACCAAGTGGGACATGGTCAGAGTTTGGGAAACAAATGCATGC 61

Db 22689 AAGTTGTGCGAGAGCAAGTGGGACATGGTCAGAGTTTGGGAAACAAATGCATGC 22630

Qy 62 AGGAACCAATCAGAAACCTTGAAGAGACGACACACGATCTTGCAACTATGTCTTCCCA 121

Db 22629 AAGATCAGTCATTAACCTTGAGGGAGCAAAACATGGATCTTGCACACTATGTCTTCCCA 22570

Qy 122 GCTCACAATATGATTGTACTTCCCAATGTTAA 154

Db 22569 GCTCACAATATGATTGTACTTCCCAATGTTAA 22537

RESULT 13

AC004747/c

LOCUS

DEFINITION

AC004747

Arabisopsis thaliana chromosome 2 clone T19L18 map B68, complete

sequence.

AC004747

VERSION

AC004747.3

KEYWORDS

HTG.

SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 87080)  
 AUTHORS Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby, M.L.,  
 Brandon, R.C., Sykes, S.M., Mason, T.M., Kerlavage, A.R., Adams, M.D.,  
 Somerville, C.R. and Venter, J.C.  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 87080)  
 AUTHORS Lin X.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712  
 Medical Center Dr., Rockville, MD 20850, USA  
 REFERENCE 3 (bases 1 to 87080)  
 AUTHORS Town, C.D. and Kaul, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-FEB-2002) The Institute for Genomic Research, 9712  
 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org  
 COMMENT On Apr 18, 2002 this sequence version replaced gi:6598441.  
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[illegible][illegible]

RESULT	14
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DEFINITION	MASC STS16438 <i>Arabidopsis thaliana</i> (Cap Verde islands-0 accession) Genomic DNA <i>Arabidopsis thaliana</i> STS genomic, sequence tagged site.
ACCESSION	BV010699
VERSION	BV010699.1 GI:32963197

Db 153 AGAATCAGTCATTAACTTGGGAGCAAAACATGGATCTTGCAACTATGCTTCCCA 212  
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## RESULT 15

BV010698 582 bp DNA linear STS 18-JUL-2003  
 LOCUS MASC STS16439 Arabidopsis thaliana (Konchezero accession) genomic  
 DEFINITION DNA Arabidopsis thaliana STS genomic, sequence tagged site.

ACCESSION BV010698  
 VERSION BV010698.1 GI:32963196  
 KEYWORDS STS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 582)  
 AUTHORS Schmidt,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,  
 Mitchell-Olds,T. and Weisshaar,B.  
 TITLE Large-Scale Identification and Analysis of Genome-Wide  
 Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana  
 Genome Res. 13 (6), 1250-1257 (2003)

JOURNAL 22683230  
 MEDLINE 12799357  
 PUBMED  
 COMMENT

Synonyms: PCP16C2\_cs22491.a  
 Contact: Karl Schmid  
 Department of Genetics and Evolution  
 Max-Planck-Institute of Chemical Ecology  
 Winzerlaer Str. 10, 07745 Jena, Germany  
 Tel: + 49-3641-571465  
 Fax: + 49-3641-571402  
 Email: schmid@ice.mpg.de  
 Primer A: CGCTGCTCTGTTCTCTTTG  
 Primer B: AAACAACCGTTGTTGGTCA  
 STS size: 582

## PCR Profile:

Presoak: 94 degrees for 2.00 minute(s)  
 Denaturation: 94 degrees for 0.50 minute(s)  
 Annealing: 58 degrees for 0.50 minute(s)  
 Polymerization: 72 degrees for 1.00 minute(s)  
 PCR Cycles: 35  
 Thermal Cycler: Perkin Elmer GeneAmp9600

## Protocol:

Template: 20 - 100 ng  
 Primer: each 1 uM  
 dNTPs: each 400 uM  
 Taq Polymerase: 0.05 units/ul  
 Total Vol: 10 ul

## Buffer:

MgCl2: 1.5 mM  
 KCl: 50 mM  
 Tris-HCl: 10 mM  
 pH: 8.3

FEATURES  
source

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 /note="Genomic DNA prepared from rosette leaves. DNA was  
 amplified and directly sequenced from both directions and  
 assembled into a consensus sequence. Note: Sequencing  
 granted in the context of the GABI Arabidopsis VerbundI:  
 Genetic Diversity, 'Establishment of high-efficiency  
 SNP-based mapping tools and development of methods for  
 genome-wide mutation detection' PIs: Thomas Altmann,

ORIGIN  
 Thomas Mitchell-Olds, Bernd Weisshaar"  
 <1..>582

Query Match 78.6%; Score 121; DB 11; Length 582;  
 Best Local Similarity 86.9%; Pred. No. 4.3e-26;  
 Matches 133; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 AGTTTGTGGAGAGACCAAGTGGGACATGGTCAGGATTTCTGGGAACAACAATGCATGC 61  
 Db 94 AAGTTTGTGGAGAGACCAAGTGGTACTTTGGTCAGGATTTGGGAACAACAATGCATGC 153  
 QY 62 AGGAACCAATGCAGAAACCTTGAAAAGAGCAGAACACGGATCTTGCAACTATATGCTTCCCA 121  
 Db 154 AAGAATCAGTCATTAACTTGAGGGAGCAGAACATGGATCTTGCAACTATGCTTCCCA 213  
 QY 122 GCTCAAAATGATTGTTGTTACTTCCCATGTTAA 154  
 Db 214 GCTCAAAAGTGATCTGTTTACGTCCCATGTTAA 246

Search completed: May 18, 2004, 17:59:04  
 Job time : 758.05 secs

This sequence represents the cDNA sequence cloned into the E. coli cassette vector pMON23317 to generate vector pMON22652. The cDNA encodes

CC the antifungal polypeptide AlyAPP, isolated from plants of the genus  
 CC Alyssum. The AlyAPP polypeptide can be used to control phytopathogenic  
 CC fungi, whilst the coding DNA can be used to produce transgenic plants  
 CC that express the polypeptide making them resistant to the phytopathogenic  
 CC fungi.

XX Sequence 270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;

Query Match 100.0%; Score 154; DB 2; Length 270;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-42;  
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 60  
 |||||  
 DB 108 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167  
 |||||

QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGCAGACACCGGATCTTGCAACTATGTCTTCCC 120  
 |||||  
 DB 168 CAGGAACCAATGCAGAAACCTTGAAGAGCAGACACCGGATCTTGCAACTATGTCTTCCC 227  
 |||||

QY 121 AGCTCACAAATGTAATTTGTACTTCCCATGTTAA 154  
 |||||  
 DB 228 AGCTCACAAATGTAATTTGTACTTCCCATGTTAA 261  
 |||||

RESULT 2  
 AAT94574  
 ID AAT94574 standard; cDNA; 286 BP.

XX AC AAT94574;

XX DT 12-MAY-1998 (first entry)

XX DE Alyssum species anti-fungal polypeptide AlyAPP cDNA sequence.

XX KW Antifungal polypeptide; AlyAPP; inhibition; transgenic plant;

XX KW phytopathogenic fungus; resistance; ss.

XX OS Alyssum sp.

XX FH Key Location/Qualifiers  
 CDS 117..269  
 FT /\*tag= a  
 FT /product= "mature AlyAPP protein"  
 FT /note= "no start codon given at 5' end of sequence"

XX WO9737024-A2.

XX PN 09-OCT-1997.

XX PD 27-MAR-1997; 97WO-US005709.

XX PF 29-MAR-1996; 96US-00627706.

XX PR (MONS ) MONSANTO CO.

XX PA Liang J, Shah D, Wu Y, Rosenberger CA;

XX PI WPI; 1997-503109/46.

XX DR P-PSDB; AAW35558.

XX CC Alyssum antifungal polypeptide and corresponding DNA - used in the  
 CC production of transgenic plants resistant to phytopathogenic fungi.

XX PS Claim 12; Page 68; 92pp; English.

XX CC This sequence encodes the mature protein of an antifungal polypeptide  
 CC (AlyAPP) isolated from plants of the genus Alyssum. The sequence was PCR  
 CC amplified using primers AAT94583-T94584, and the resultant 264 bp  
 CC fragment was cloned as a BamHI fragment into the expression vector  
 CC pMON2317 to generate plasmid pMON22652. The AlyAPP sequence in this  
 CC plasmid is placed under control of an E35S promoter and the maize HSP70  
 CC intron I sequence. The protein can be used to control phytopathogenic

CC fungi, whilst the DNA can be used to produce transgenic plants that  
 CC express the protein making them resistant to the phytopathogenic fungi

XX Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 2; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 2e-42;  
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 60  
 |||||  
 DB 116 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 175  
 |||||

QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGCAGACACCGGATCTTGCAACTATGTCTTCCC 120  
 |||||  
 DB 176 CAGGAACCAATGCAGAAACCTTGAAGAGCAGACACCGGATCTTGCAACTATGTCTTCCC 235  
 |||||

QY 121 AGCTCACAAATGTAATTTGTACTTCCCATGTTAA 154  
 |||||  
 DB 236 AGCTCACAAATGTAATTTGTACTTCCCATGTTAA 269  
 |||||

RESULT 3  
 AAT9289  
 ID AAT9289 standard; DNA; 481 BP.

XX AC AAT9289;

XX DT 12-MAY-1998 (first entry)

XX DE Alyssum species AlyAPP cDNA sequence.

XX KW Antifungal polypeptide; AlyAPP; inhibition; transgenic plant;

XX KW phytopathogenic fungus; resistance; ss.

XX OS Alyssum sp.

XX FH Key Location/Qualifiers  
 CDS 53..292  
 FT /\*tag= a  
 FT /product= "AlyAPP antifungal polypeptide"  
 FT /\*tag= b  
 FT mat\_peptide 140..289  
 FT /\*tag= c  
 FT polyA\_signal 439..443  
 FT /\*tag= d

XX PN WO9737024-A2.

XX PD 09-OCT-1997.

XX PF 27-MAR-1997; 97WO-US005709.

XX PR 29-MAR-1996; 96US-00627706.

XX PR (MONS ) MONSANTO CO.

XX PA Liang J, Shah D, Wu Y, Rosenberger CA;

XX PI WPI; 1997-503109/46.

XX DR P-PSDB; AAW35560.

XX CC Alyssum antifungal polypeptide and corresponding DNA - used in the  
 CC production of transgenic plants resistant to phytopathogenic fungi.

XX PS Example 4; Fig 1; 92pp; English.

XX CC This sequence represents the cDNA sequence which encodes the antifungal  
 CC polypeptide AlyAPP, isolated from plants of the genus Alyssum. The AlyAPP  
 CC polypeptide can be used to control phytopathogenic fungi, whilst the  
 CC coding DNA can be used to produce transgenic plants that express the  
 CC polypeptide making them resistant to the phytopathogenic fungi



SQ Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;  
 Query Match 100.0%; Score 154; DB 2; Length 481;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-42;  
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTCTGCGAGAGCAAGTGGGACATGTCAGGAGTTGTGGGAAACAATGCATG 60  
 DB 139 AAGTTCTGCGAGAGCAAGTGGGACATGTCAGGAGTTGTGGGAAACAATGCATG 198  
 QY 61 CAGGAACCAATGCAGAAACCTTTGAAAGAGCAGACACGGATCTTGCAACTATGCTTCCC 120  
 DB 199 CAGGAACCAATGCAGAAACCTTTGAAAGAGCAGACACGGATCTTGCAACTATGCTTCCC 258  
 QY 121 AGCTCACAATGTATTTGTTACTTCCCATGTTAA 154  
 DB 259 AGCTCACAATGTATTTGTTACTTCCCATGTTAA 292

RESULT 4  
 AAT94581  
 ID AAT94581 standard; DNA; 500 BP.  
 AC AAT94581;  
 XX  
 DT 12-MAY-1998 (first entry)  
 XX  
 DE Composite cDNA sequence for Alyssum species antifungal polypeptide.  
 XX  
 KW Antifungal polypeptide; AlyAPP; inhibition; transgenic plant;  
 KW phytopathogenic fungus; resistance; ss.  
 XX  
 OS Alyssum sp.  
 XX  
 PN WO9737024-A2.  
 XX  
 PD 09-OCT-1997.  
 XX  
 PF 27-MAR-1997; 97WO-US005709.  
 XX  
 PR 29-MAR-1996; 96US-00627706.  
 XX  
 PA (MONS ) MONSANTO CO.  
 XX  
 PI Liang J, Shah D, Wu Y, Rosenberger CA;  
 XX  
 DR WPI; 1997-503109/46.  
 XX  
 PT Alyssum antifungal polypeptide and corresponding DNA - used in the  
 PT production of transgenic plants resistant to phytopathogenic fungi.  
 XX  
 PS Example 4; Page 67; 92pp; English.  
 XX  
 CC This sequence represents the cDNA sequence encoding the antifungal  
 CC polypeptide AlyAPP, from plants of the genus Alyssum. The sequence  
 CC represents a composite of the sequences isolated by 5' and 3' RACE (Rapid  
 CC Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The  
 CC AlyAPP polypeptide can be used to control phytopathogenic fungi, whilst  
 CC the coding DNA can be used to produce transgenic plants that express the  
 CC polypeptide making them resistant to the phytopathogenic fungi  
 XX  
 SQ Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;

Query Match 91.0%; Score 140.2; DB 2; Length 500;  
 Best Local Similarity 94.8%; Pred. No. 1.3e-37;  
 Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGCAAGTGGGACATGTCAGGAGTTGTGGGAAACAATGCATGC 61  
 DB 159 AAGTTGTGCGAGAGTCCAAAGTGGGACATGTCAGGAGTTGTGGGAAATAATACGCATGC 218  
 QY 62 AGGAACCAATGCAGAAACCTTTGAAAGAGCAGACACGGATCTTGCAACTATGCTTCCCA 121

Db 219 AGGAACCAATGCAGAAACCTTTGAAAGAGCAGACACGGATCTTGCAACTATGCTTCCCA 278  
 QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154  
 DB 279 GCTCACAATGTATTTGTTACTTCCCATGTTAA 311

RESULT 5  
 ADC51221  
 ID ADC51221 standard; DNA; 394 BP.  
 XX  
 AC ADC51221;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Brassica oleracea defensin protein coding sequence.  
 XX  
 KW antimicrobial protein; defensin; transgenic plant;  
 KW composite disease resistance; pathogenic bacteria;  
 KW rice white leaf blight; brown-stripe disease; glume blight;  
 KW seedling damping-off disease; filamentous fungi; rice blight;  
 KW sheath blight disease; leaf blight; gene; ds.  
 XX  
 OS Brassica oleracea.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..243  
 FT /\*tag= a  
 FT /product= "Brassica oleracea defensin protein"  
 PN JP2003088379-A.  
 XX  
 PD 25-MAR-2003.  
 XX  
 PF 18-SEP-2001; 2001JP-00283117.  
 XX  
 PR 18-SEP-2001; 2001JP-00283117.  
 XX  
 PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
 XX  
 DR WPI; 2003-621123/59.  
 DR P-PSDB; ADC51222.  
 XX  
 PT Novel protein from Brassica campestris, useful as antimicrobial against  
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for  
 PT treating e.g. rice white leaf blight and sheath blight disease.  
 XX  
 PS Claim 3; SEQ ID NO 1; 34pp; Japanese.  
 XX  
 CC The invention comprises the amino acid and coding sequences of  
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein  
 CC sequences of the invention are useful for producing transformed plants  
 CC with composite disease resistance, especially resistant to diseases  
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-  
 CC stripe disease, glume blight, and seedling damping-off disease. As well  
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath  
 CC blight disease, and leaf blight. The present DNA sequence encodes a  
 CC Brassica defensin protein of the invention.  
 XX  
 SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Query Match 79.6%; Score 122.6; DB 9; Length 394;  
 Best Local Similarity 87.6%; Pred. No. 1.2e-31;  
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGCAAGTGGGACATGTCAGGAGTTGTGGGAAACAATGCATGC 61  
 DB 91 AAGTTGTGCGAGAGGCCAAAGTGGGACATGTCAGGAGTTGTGGAAACATAACGCATGC 150  
 QY 62 AGGAACCAATGCAGAAACCTTTGAAAGAGCAGACACGGATCTTGCAACTATGCTTCCCA 121  
 DB 151 AAGAATCAGTGCATTAACCTTGAAGAAACGACATGATCTTGCAACTATGCTTCCCA 210

QY 122 GCTCACAAGTATTTGTTACTTCCCATGTAA 154  
 Db 211 GCTCACAAGTATTTGTTACTTCCCATGTAA 243

RESULT 6  
 ADC51223  
 ID ADC51223 standard; DNA; 426 BP.

XX AC AC  
 XX ADC51223;  
 DT 18-DEC-2003 (first entry)  
 XX DE Brassica defensin protein coding sequence.

XX antimicrobial protein; defensin; transgenic plant;  
 KW composite disease resistance; pathogenic bacteria;  
 KW rice white leaf blight; brown-stripe disease; glume blight;  
 KW seedling damping-off disease; filamentous fungi; rice blight;  
 KW sheath blight disease; leaf blight; gene; ds.

OS Brassica sp.  
 FH Key Location/Qualifiers  
 FT CDS 1..243  
 FT /\*tag= a  
 FT /product= "Brassica defensin protein"

XX JF2003088379-A.

XX 25-MAR-2003.

XX 18-SEP-2001; 2001JP-00283117.

XX 18-SEP-2001; 2001JP-00283117.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2003-621123/59.

XX P-PSDB; ADC51224.

XX Novel protein from Brassica campestris, useful as antimicrobial against  
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for  
 PT treating e.g. rice white leaf blight and sheath blight disease.

XX Claim 3; SEQ ID NO 3; 34pp; Japanese.

XX The invention comprises the amino acid and coding sequences of  
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein  
 CC sequences of the invention are useful for producing transformed plants  
 CC with composite disease resistance, especially resistant to diseases  
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-  
 CC stripe disease, glume blight, and seedling damping-off disease. As well  
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath  
 CC blight disease, and leaf blight. The present DNA sequence encodes a  
 CC Brassica defensin protein of the invention.

XX Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;

Query Match 79.6%; Score 122.6; DB 9; Length 426;  
 Best Local Similarity 87.6%; Pred. No. 1.3e-31;  
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGGATTTGTGGACACATGATGC 61  
 Db 91 AGTTGTGCGAGAGCCAAAGTGGGACATGTCAGGATTTGTGGACACATGATGC 150

QY 62 AGGAACCAATGCAAAACCTTTGAAAGACGAGAACACCGATCTTGCACATGATGCTTCCCA 121  
 Db 151 AAGATCAGTGCATTAACCTTTGAGAAAGCAGACATGATCTTGCACATGATGCTTCCCA 210

QY 122 GCTCACAAGTATTTGTTACTTCCCATGTAA 154

Db 211 GCTCACAAGTATTTGTTACTTCCCATGTAA 243

RESULT 7

ADA68378

ID ADA68378 standard; DNA; 243 BP.

XX AC ADA68378;

XX 20-NOV-2003 (first entry)

XX Arabidopsis thaliana gene, SEQ ID 747.

XX Plant; bacterial infection; fungal infection; viral infection; ds.

XX Arabidopsis thaliana.

XX WO2003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
 XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to  
 PT pathogenic infection for conferring resistance or tolerance to a plant to  
 PT bacterial, fungal or viral infection by determining or detecting plant  
 PT gene expression.

XX Claim 6; SEQ ID NO 747; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes  
 CC involved in plant resistance or response to pathogenic infection. M1  
 CC comprises identifying a gene whose expression is significantly altered in  
 CC the incompatible interaction of plant gene expression relative to  
 CC expression of the gene in an uninfected plant, in a mutant plant that  
 CC does not express a gene associated with response to pathogenic infection,  
 CC or in a corresponding incompatible or compatible interaction. (M1) is  
 CC useful for conferring resistance to resistance or tolerance to a plant to  
 CC bacterial, fungal or viral infection. The present sequence was used to  
 CC illustrate the invention.

XX Sequence 243 BP; 58 A; 56 G; 59 G; 70 T; 0 U; 0 Other;

Query Match 77.5%; Score 119.4; DB 7; Length 243;  
 Best Local Similarity 86.3%; Pred. No. 1.3e-30;  
 Matches 132; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGGATTTGTGGACACATGATGC 61  
 Db 91 AGTTGTGCGAGAGCCAAAGTGGGACATGTCAGGATTTGTGGACACATGATGC 150

QY 62 AGGAACCAATGCAAAACCTTTGAAAGACGAGAACACCGATCTTGCACATGATGCTTCCCA 121  
 Db 151 AAGAATCAGTGCATTAACCTTTGAGAAAGCAGACATGATCTTGCACATGATGCTTCCCA 210

QY 122 GCTCACAAGTATTTGTTACTTCCCATGTAA 154

Db 211 GCTCACAAGTATCTGCTACTTCCCATGTAA 243

RESULT 8

AAV10632

ID AAV10632 standard; DNA; 403 BP.

```
XX AAV10632;
AC
XX 23-JUN-1998 (first entry)
DT
XX
XX A. thaliana PDF1.1 DNA.
DE
XX
XX Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
KW fungi; ss.
XX
XX Arabidopsis thaliana.
OS
XX
XX Key Location/Qualifiers
FH CDS 26..268
FT /*tag= a
FT sig_peptide 26..113
FT /*tag= b
FT mat_peptide 114..265
FT /*tag= c
FT /*product= "PDF1.1"
FT /*note= "plant defensin"
XX
XX WO9800023-A2.
PN
XX
XX 08-JAN-1998.
PD
XX
XX 20-JUN-1997; 97WO-GB001672.
PF
XX
XX 01-JUL-1996; 96GB-00013753.
PR
XX
XX (ZENE ) ZENECA LTD.
PA
XX
XX Broekaert WF, Thomma BPHJ, Penminckx IAMA, Terras FRG, Manners JM;
PI Kazan K;
PI
XX
XX WPI; 1998-086663/08.
DR
XX P-FSDB; AAW40345.
DR
XX
XX Protecting plants against pathogens by inducing defensin genes - by
PT stimulating ethylene or jasmonate pathways, also new promoter of defensin
PT gene from Arabidopsis.
XX
XX Disclosure; Fig 1; 72pp; English.
PS
XX
XX This sequence encodes the Arabidopsis PDF1.1 gene which is used in a
CC novel method for the protection of plants against pathogens which
CC involves inducing expression of a plant defensin gene by stimulating the
CC jasmonate and/or ethylene pathways. The method is used to induce
CC protection against necrotrophic pathogens, specifically fungi and does
CC not require cytotoxic or potentially harmful chemicals
XX
XX Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
SQ
XX
XX Query Match 77.5%; Score 119.4; DB 2; Length 403;
XX Best Local Similarity 86.3%; Pred. No. 1.5e-30;
XX Matches 132; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
XX
XX 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAAACAACAATGCATGC 61
XX |
XX 116 AAGTTGTGCGAGAGCCAAAGTGGGACATGGTCAGGAGTTTGTGGGAAACAAGTACCGCGTGC 175
XX |
XX 62 AGGAACCAATGCAGAAACCTTGAAGAGAGACGAGTCTTGCAACTATGCTTCCCA 121
XX |
XX 176 AAGATCATGTCATTAACCTTGAGAAAGCAGCATGGATCTTGCAACTATGCTTCCCA 235
XX |
XX 122 GCTCACAATGATTTGTTACTTCCCATGTTAA 154
XX |
XX 236 GCTCACAATGATTTGTTACTTCCCATGTTAA 268
XX
XX RESULT 9
XX ABQ82690
XX ID ABQ82690 standard; cDNA; 243 BP.
```

```
XX ABQ82690;
AC
XX 02-JAN-2003 (first entry)
DT
XX
XX Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1.
DE
XX
XX Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
KW ss.
XX
XX Eutrema wasabi.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..243
FT /*tag= a
FT /*product= "gamma-thionin"
XX
XX JP2002272292-A.
PN
XX
XX 24-SEP-2002.
PD
XX
XX 22-MAR-2001; 2001JP-00083526.
PF
XX
XX 22-MAR-2001; 2001JP-00083526.
PR
XX
XX (IWAT-) IWATE KEN.
PA
XX
XX WPI; 2002-718704/78.
DR
XX P-FSDB; ABP53725.
DR
XX
XX A disease-resistant plant in which wasabi gamma-thionin gene is
PT introduced, creation of the disease-resistant plant.
PT
XX
XX Claim 3; Page 8; 11pp; Japanese.
XX
XX The present invention describes a disease-resistant plant in which a
CC wasabi gamma-thionin gene is introduced. Also described is a method for
CC the creation of the above disease-resistant plant by introducing a wasabi
CC gamma-thionin gene to a plant. The present sequence encodes a Eutrema
CC wasabi (Wasabia japonica) gamma-thionin protein from the present
CC invention
XX
XX Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;
SQ
XX
XX Query Match 76.5%; Score 117.8; DB 6; Length 243;
XX Best Local Similarity 85.6%; Pred. No. 4.4e-30;
XX Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
XX
XX 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAAACAACAATGCATGC 61
XX |
XX 91 AAGTTGTGCGAGAGTCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAACAATCGGTGC 150
XX |
XX 62 AGGACCAATGCAGAAACCTTGAAGAGACGAGTCTTGCAACTATGCTTCCCA 121
XX |
XX 151 AAGATCATGTCATTAACCTTGAGGAGACGACATGGATCTTGCAACTATGCTTCCCA 210
XX |
XX 122 GCTCACAATGATTTGTTACTTCCCATGTTAA 154
XX |
XX 211 TATCAGATGATCTGTTACTTCCCATGTTAA 243
XX
XX RESULT 10
XX ABZ14241
XX ID ABZ14241 standard; DNA; 243 BP.
XX
XX AC ABZ14241;
XX
XX 21-JAN-2003 (first entry)
DT
XX
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2046.
DE
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
```

OS Arabidopsis thaliana.  
 PN WO200216655-A2.  
 PD 28-FEB-2002.  
 PF 24-AUG-2001; 2001WO-US026685.  
 PR 24-AUG-2000; 2000US-0227866P.  
 PR 26-JAN-2001; 2001US-0264647P.  
 PR 22-JUN-2001; 2001US-0300111P.  
 XX (SCRI ) SCRIPPS RES INST.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX Harper JF, Kreps J, Wang X, Zhu T;  
 PI WPI; 2002-304127/34.  
 DR Identifying a stress condition to which a plant cell has been exposed and  
 XX producing plants with increased tolerance to these abiotic stresses.  
 PT Claim 144; SEQ ID NO 246; 577pp + Sequence Listing; English.  
 PS The invention relates to identifying a stress condition to which a plant  
 CC cell has been exposed, comprising: (a) contacting nucleic acid  
 CC representative of expressed polynucleotides in the plant cell with an  
 CC array or probes representative of the plant cell genome; and (b)  
 CC detecting a profile of expressed polynucleotides in the plant cell  
 CC characteristic of a stress response. The method is useful in the  
 CC production of transgenic plants, cells and seeds and in producing plants  
 CC with increased tolerance to abiotic stress. The present sequence is that  
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
 CC in methods of the invention. Note: The sequence data for this patent is  
 CC not represented in the printed specification but is based on sequence  
 CC information supplied to Derwent by the European Patent Office  
 XX  
 XX Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;

Query Match 76.5%; Score 117.8; DB 6; Length 243;  
 Best Local Similarity 85.8%; Pred. No. 4.4e-30;  
 Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
 QY 2 AGTTTGTGCGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGATGC 61  
 Db 91 AAGTTGTGCGAGAGCCAAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGATGC 150  
 QY 62 AGGAACCAATGCGAGAACCTTGAAGAGCAGAACACGGATCTTGGCAACTATGCTTCCCA 121  
 Db 151 AAGAATCAGTGCATTAACTTGAAGAGGCCAACAATGATGCATGCAACTATGCTTCCCA 210  
 QY 122 GCTCACAATGATTTGTACTTCCCATGTAA 154  
 Db 211 GCACACAGTATCTGTACGTCCTCATGTAA 243

RESULT 11  
 ABZ42136  
 ID ABZ42136 standard; cDNA; 243 BP.  
 XX  
 AC ABZ42136;  
 XX  
 XX 27-FEB-2003 (first entry)  
 DT Arabidopsis thaliana gene #120 modulated by PTGS.  
 DE Arabidopsis thaliana.  
 XX Posttranscriptional gene silencing; PTGS; plant; transformation; gene;  
 KW ss.  
 XX Arabidopsis thaliana.  
 OS  
 XX Key Location/Qualifiers  
 FH 1. .243  
 FT CDS

FT  
 XX WO200281695-A2.  
 PN 17-OCT-2002.  
 PD 05-APR-2002; 2002WO-EP003806.  
 PF 06-APR-2001; 2001US-0282049P.  
 PR (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 PA (FRIE-) FRIEDRICH MIESCHER INST.  
 XX Zhu T, Glazov EA, Meins F, Wang X, Chang H;  
 PI WPI; 2003-103337/09.  
 DR P-PSDB; ABP81292.  
 DR Novel polynucleic acid segment useful for modulating gene expression  
 PT within a cell by posttranscriptional gene silencing, and for augmenting a  
 XX plant cell genome.  
 PS Claim 18; Page 425-426; 438pp; English.  
 CC The invention relates to a novel isolated polynucleic acid segment  
 CC modulated within a cell by posttranscriptional gene silencing (PTGS). The  
 CC invention specifically relates to a method to identify an expression  
 CC product that is modulated by PTGS. The polynucleotide is useful for  
 CC modulating the gene expression within a cell by PTGS, by introducing the  
 CC polynucleic acid into a cell and expressing the nucleic acid segment in  
 CC the cell to form a product. The polynucleic acid segment is also useful  
 CC for augmenting a cell genome, and for augmenting a plant genome, by  
 CC contacting a plant cell with the segment to produce a transformed plant  
 CC cell, and growing the transformed plant cell to produce a differentiated  
 CC transformed plant. The sequences shown in ABZ42017 - ABZ42142 represent  
 CC segments of A. thaliana cDNA modulated by PTGS  
 XX  
 XX Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;

Query Match 76.5%; Score 117.8; DB 7; Length 243;  
 Best Local Similarity 85.6%; Pred. No. 4.4e-30;  
 Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
 QY 2 AGTTTGTGCGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGATGC 61  
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 QY 62 AGGAACCAATGCGAGAACCTTGAAGAGCAGAACACGGATCTTGGCAACTATGCTTCCCA 121  
 Db 151 AAGAATCAGTGCATTAACTTGAAGAGGCCAACAATGATGCATGCAACTATGCTTCCCA 210  
 QY 122 GCTCACAATGATTTGTACTTCCCATGTAA 154  
 Db 211 GCACACAGTATCTGTACGTCCTCATGTAA 243

RESULT 12  
 AAV10633  
 ID AAV10633 standard; DNA; 400 BP.  
 XX  
 AC AAV10633;  
 XX  
 XX 23-JUN-1998 (first entry)  
 DT A. thaliana PDF1.2 DNA.  
 DE Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;  
 KW fungi; ss.  
 XX Arabidopsis thaliana.  
 OS  
 XX Key Location/Qualifiers  
 FH 32. .274  
 FT CDS

FT sig\_peptide /\*tag= a  
 FT 32..119 /\*tag= b  
 FT mat\_peptide 120..271 /\*tag= c  
 FT /product= "PDF1.2"  
 FT /note= "plant defensin"  
 XX

XX W09800023-A2.

XX 08-JAN-1998.

XX 20-JUN-1997; 97WO-GB001672.

XX 01-JUL-1996; 96GB-00013753.

XX (ZENE ) ZENECA LTD.

XX Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM;  
 XX Kazan K;

XX WPI; 1998-086663/08.

XX P-PSDB; AAW40346.

XX Protecting plants against pathogens by inducing defensin genes - by  
 XX stimulating ethylene or jasmonate pathways, also new promoter of defensin  
 XX gene from Arabidopsis.

XX Disclosure; Fig 1; 72pp; English.

XX This sequence encodes the Arabidopsis PDF1.2 gene which is used in a  
 XX novel method for the protection of plants against pathogens which  
 XX involves inducing expression of a plant defensin gene by stimulating the  
 XX jasmonate and/or ethylene pathways. The method is used to induce  
 XX protection against necrotrophic pathogens, specifically fungi and does  
 XX not require cytotoxic or potentially harmful chemicals

XX Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;

Query Match 76.5%; Score 117.8; DB 2; Length 400;  
 Best Local Similarity 85.6%; Pred. No. 5.4e-30;  
 Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACATGCGATGC 61

DB 122 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACATGCGATGC 181

QY 62 AGGAACCAATGCAGAAACCTTGAAGAGACGAGAACACGGATCTTGCATATGTCTTCCCA 121

DB 182 AAGAATCAGTGCATTACCTTTGAAGAGAGCCAAACATGATCATGCAACTATGTCTTCCCA 241

QY 122 GCTCACAATGTATTGTACTTCCCATGTTAA 154

DB 242 GCACACAAGTGTATCTGTACTTCCCATGTTAA 274

RESULT 13

AAQ38650  
 ID AAQ38650 standard; DNA; 414 BP.

XX AC AAQ38650;

XX 25-MAR-2003 (revised)

XX 07-JUL-1993 (first entry)

XX Rs-APF1 cDNA.

XX Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;  
 KW fungicide; bacteriocide; antibiotic; antifungal; gram positive;  
 KW plant disease resistance; low toxicity.

XX Raphanus sativus.

XX

PH Key Location/Qualifiers  
 FT CDS 16..256  
 FT /\*tag= a

XX W09305153-A1.

XX 18-MAR-1993.

XX 27-AUG-1992; 92WO-GB001570.

XX 29-AUG-1991; 91GB-00018523.

XX 13-FEB-1992; 92GB-00003038.

XX 25-JUN-1992; 92GB-00013526.

XX (ICIL ) IMPERIAL CHEM IND PLC.

XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;

XX Vanderleyden J;

XX WPI; 1993-100978/12.

XX Biocidal proteins isolated from seeds of plants - e.g. brassica or  
 XX dahlia, useful for increasing plants' resistance to fungal and bacterial  
 XX diseases.

XX Example 21; Fig 35; 110pp; English.

XX This cDNA represents the sequence of Rs-APF1 from Raphanus sativus. PCR  
 XX primer AAQ38640 was used together with AAQ38641 to generate a probe for  
 XX screening a Raphanus sativus seed cDNA library. This primer corresponds  
 XX to amino acids 2 to 7 of Rs-APF1 and has a sense orientation. The 144bp  
 XX product was partially re-amplified using AAQ38642 and AAQ38641 to give a  
 XX 123bp product, which was further re-amplified with the same primers and  
 XX digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR  
 XX product. This was used to screen a lambda ZAPII cDNA library by in situ  
 XX plaque hybridisation. Positive plaques were purified and subjected to two  
 XX additional screening rounds with the same probe. Inserts were excised in  
 XX vivo into the pBluescript phagemid form with the aid of helper phage  
 XX R408. Inserts from 22 positive clones were excised by EcoRI digestion and  
 XX their size compared by agarose gel electrophoresis. Four clones had  
 XX insert sizes of approx. 400bp the others between 250-300bp. The inserts  
 XX of the 4 largest clones were then sequenced and found to differ only in  
 XX the length of their 5' and 3' UTR's. The longest sequence is given here.  
 XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 76.5%; Score 117.8; DB 2; Length 414;  
 Best Local Similarity 85.6%; Pred. No. 5.5e-30;  
 Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACATGCGATGC 61

DB 106 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACATGCGATGC 165

QY 62 AGGAACCAATGCAGAAACCTTGAAGAGACGAGAACACGGATCTTGCATATGTCTTCCCA 121

DB 166 AAGAATCAGTGCATTACCTTTGAAGAGACGAGACATGATCTTGCATATGTCTTCCCA 225

QY 122 GCTCACAATGTATTGTACTTCCCATGTTAA 154

DB 226 GCTCACAAGTGTATCTGTACTTCTTCTTGTAA 258

RESULT 14

AAQ70128  
 ID AAQ70128 standard; cDNA; 414 BP.

XX AC AAQ70128;

XX 25-MAR-2003 (revised)

XX 14-FEB-1995 (first entry)

XX

```

DE Antimicrobial Rs-APPI.
XX
XX Antimicrobial; Rs-APPI; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
XX
XX Raphanus sativus.
OS
XX WO9416076-A1.
PN
XX 21-JUL-1994.
PD
XX
XX 05-JAN-1994; 94WO-GB0000012.
PF
XX
XX 08-JAN-1993; 93GB-00000281.
PR
XX
XX (ZENE ) ZENECA LTD.
PA
XX Dubock AC, Powell KA, Rees SB;
PI WPI; 1994-249223/30.
XX P-PSDB; AAR57325.
XX
XX Antimicrobial protein producing endo-symbiotic microorganisms - is
PT produced by combining nucleic acids encoding the protein with an
XX endophyte, useful for protecting plant hosts from esp. fungal disease.
XX
XX Disclosure; Page 31; 39pp; English.
XX
XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
CC Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with
CC recombinant Cxc are protected against fungal disease. A suitable
CC antimicrobial protein is Rs-APPI from R. sativus. The full-length cDNA
CC sequence of Rs-APPI is given in AAQ70128. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
SQ
Query Match 76.5%; Score 117.8; DB 2; Length 414;
Best Local Similarity 85.6%; Pred. No. 5.5e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGACACAATGCATGC 61
DB 106 AAGTTGTGCGAAGGCGCAAGTGGGACATGTCAGGAGTTGTGGGACACAATGCATGC 165
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGAGTCTTGCAACTATGCTTCCCA 121
DB 166 AAGATCAGTGCATTAACTTGAAGAGCAGACATGATGATGCAACTATGCTTCCCA 225
QY 122 GCTCACAATGTATTTGTTACTTCCCATGTAA 154
DB 226 GCTCACAAGTGTATCTGCTACTTTCCTTGTAA 258
RESULT 15
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ID AAT72333 standard; cDNA; 414 BP.
XX
XX AAT72333;
AC
XX
XX 25-MAR-2003 (revised)
DT 19-JAN-1998 (first entry)
XX
XX Raphanus sativus antifungal protein I (Rs-APPI) cDNA.
XX
XX Antifungal protein; candida; fungal resistance; food additive; radish;
KW crop protection; plant defense; bacterial protection; preservative; ss.
XX
XX Raphanus sativus.
OS
XX
XX Key Location/Qualifiers
FH 16..258
FT /*tag= a

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FT /transl_except= (pos:85..87, aa:Glu)
XX sig_peptide 16..102
FT /*tag= b
XX mat_peptide 103..125
FT /*tag= c
XX /product= "antifungal_protein_1"
XX WO9721815-A2.
PN
XX 19-JUN-1997.
PD
XX
XX 12-DEC-1996; 96WO-GB003068.
PF
XX
XX 13-DEC-1995; 95GB-00025455.
PR
XX 28-MAR-1996; 96GB-00006552.
XX
XX (ZENE ) ZENECA LTD.
PA
XX Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;
XX Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
XX Van Gelder WMJ;
XX
XX WPI; 1997-332786/30.
DR P-PSDB; AAW19280.
XX
XX Antifungal peptide derived from radish antifungal protein 2 - and related
XX DNA, useful for producing plants with increased fungal resistance and as
XX therapeutic or preservative agent.
XX
XX Claim 8; Fig 2; 65pp; English.
XX
XX This cDNA sequence encodes an Rhanus sativus (radish) antifungal
XX protein (Rs-APPI). Analogues of the homologous protein, Rs-AP2
XX (AAW19281), have also been produced (see AAW19282-92, AAW19294-98,
XX AAW19301-04, AAW19330-34 and AAW1765-834). Plants containing DNA
XX sequences encoding these proteins have improved resistance to fungi.
XX Compositions containing the peptides can be used to control fungi or
XX bacteria in pharmaceutical (e.g. treatment of Candida infections) or
XX preservative purposes (as food additives). In agriculture, the peptide
XX may be used to improve disease resistance or disease tolerance of crops,
XX either pre or post harvest. When applied to plants they may also have
XX curative as well as protective actions. The peptides may also be used to
XX protect plants by introducing them, or a microorganism capable of
XX expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
XX PI field.)
XX
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
SQ
Query Match 76.5%; Score 117.8; DB 2; Length 414;
Best Local Similarity 85.6%; Pred. No. 5.5e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGACACAATGCATGC 61
DB 106 AAGTTGTGCGAAGGCGCAAGTGGGACATGTCAGGAGTTGTGGGACACAATGCATGC 165
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGAGTCTTGCAACTATGCTTCCCA 121
DB 166 AAGATCAGTGCATTAACTTGAAGAGCAGACATGATGATGCAACTATGCTTCCCA 225
QY 122 GCTCACAATGTATTTGTTACTTCCCATGTAA 154
DB 226 GCTCACAAGTGTATCTGCTACTTTCCTTGTAA 258
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Job time : 151.15 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:08:11 ; Search time 31.5 Seconds  
(without alignments)  
2713.093 Million cell updates/sec

Title: US-10-681-972-12\_COPY\_116\_269

Perfect score: 154

Sequence: 1 aaggtgtgcgagagaccaa.....ttgttacttcccatgtaa 154

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
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5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	154	100.0	270	1	US-08-627-706-14
2	154	100.0	270	3	US-09-103-489-14
3	154	100.0	270	4	US-09-829-381D-14
4	154	100.0	286	1	US-08-627-706-12
5	154	100.0	286	3	US-09-103-489-12
6	154	100.0	286	4	US-09-829-381D-12
7	140.2	91.0	500	1	US-08-627-706-9
8	140.2	91.0	500	3	US-09-103-489-9
9	140.2	91.0	500	4	US-09-829-381D-9
10	117.8	76.5	414	1	US-08-377-687-48
11	117.8	76.5	414	1	US-08-377-192-48
12	117.8	76.5	414	3	US-08-971-982-48
13	117.8	76.5	414	4	US-09-077-951-19
14	117.8	76.5	414	4	US-09-077-948A-45
15	115.4	74.9	308	1	US-08-627-706-5
16	115.4	74.9	308	3	US-09-103-489-5
17	115.4	74.9	308	4	US-09-829-381D-5
18	113	73.4	288	1	US-08-377-687-58
19	113	73.4	288	1	US-08-777-192-58
20	113	73.4	288	3	US-08-971-982-58
21	110.6	71.8	306	1	US-08-627-706-8
22	110.6	71.8	306	3	US-09-103-489-8
23	110.6	71.8	306	4	US-09-829-381D-8
24	109.2	70.9	285	1	US-08-627-706-16
25	109.2	70.9	285	3	US-09-103-489-16
26	109.2	70.9	285	4	US-09-829-381D-16
27	102.8	66.8	285	1	US-08-627-706-17

28 102.8 66.8 285 3 US-09-103-489-17 Sequence 17, Appl  
29 102.8 66.8 285 4 US-09-829-381D-17 Sequence 17, Appl  
30 75.8 49.2 284 1 US-08-377-687-50 Sequence 50, Appl  
31 75.8 49.2 284 1 US-08-777-192-50 Sequence 50, Appl  
32 75.8 49.2 284 3 US-08-971-982-50 Sequence 50, Appl  
33 42.4 27.5 565 4 US-09-589-733C-6 Sequence 6, Appl  
34 39.8 25.8 150 1 US-08-377-687-31 Sequence 31, Appl  
35 39.8 25.8 150 1 US-08-377-687-33 Sequence 33, Appl  
36 39.8 25.8 150 1 US-08-377-687-34 Sequence 34, Appl  
37 39.8 25.8 150 1 US-08-777-192-31 Sequence 31, Appl  
38 39.8 25.8 150 1 US-08-777-192-33 Sequence 33, Appl  
39 39.8 25.8 150 1 US-08-777-192-34 Sequence 34, Appl  
40 39.8 25.8 150 3 US-08-971-982-31 Sequence 31, Appl  
41 39.8 25.8 150 3 US-08-971-982-33 Sequence 33, Appl  
42 39.8 25.8 150 3 US-08-971-982-34 Sequence 34, Appl  
43 35.8 23.2 147 1 US-08-377-687-36 Sequence 36, Appl  
44 35.8 23.2 147 1 US-08-777-192-36 Sequence 36, Appl  
45 35.8 23.2 147 3 US-08-971-982-36 Sequence 36, Appl

#### ALIGNMENTS

RESULT 1  
US-08-627-706-14  
; Sequence 14, Application US/08627706  
; Patent No. 5773696  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yornie S.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F  
; STREET: 700 Chesterfield Village Parkway No. 5773696th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/627,706  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21(10700)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6224  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 270 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-627-706-14

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Best Local Similarity 100.0%; Pred. No. 2.8e-42;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 154  
Db 228 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 261  
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; Patent No. 6215048  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yinnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. 6215048th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/103,489  
; FILING DATE: 24-JUN-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 537-6224  
; TELEFAX: (314) 537-6047  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 270 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-103-489-14

Query Match 100.0%; Score 154; DB 3; Length 270;  
Best Local Similarity 100.0%; Pred. No. 2.8e-42;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 CAGGACCAATGCAGAAACCTTGAAGAGCAGACACGATCTTGCAACTATGTCTTCCC 120  
Db 168 CAGGACCAATGCAGAAACCTTGAAGAGCAGACACGATCTTGCAACTATGTCTTCCC 227  
QY 121 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 154  
Db 228 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 261

RESULT 3

US-09-829-381D-14  
; Sequence 14, Application US/09829381D  
; Patent No. 6653280  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yinnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Plant Pathogenic Fungi  
; FILE REFERENCE: 38-21 (10700) C  
; CURRENT APPLICATION NUMBER: US/09/829,381D  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/103,489  
; PRIOR FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 14  
; LENGTH: 270  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid  
US-09-829-381D-14  
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Best Local Similarity 100.0%; Pred. No. 2.8e-42;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 60  
Db 108 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 167  
QY 61 CAGGACCAATGCAGAAACCTTGAAGAGCAGACACGATCTTGCAACTATGTCTTCCC 120  
Db 168 CAGGACCAATGCAGAAACCTTGAAGAGCAGACACGATCTTGCAACTATGTCTTCCC 227  
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Db 228 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 261

RESULT 4  
US-08-627-706-12  
; Sequence 12, Application US/08627706  
; Patent No. 5773696  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yinnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. 5773696th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,706  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565



REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 286 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-627-706-12

Query Match 100.0%; Score 154; DB 1; Length 286;  
Best Local Similarity 100.0%; Pred. No. 2.9e-42;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 116 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 175  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACACTATGCTTCCC 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACACTATGCTTCCC 235  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 121 AGCTCACAATGTATTGTTACTTCCCATGTTAA 154  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 236 AGCTCACAATGTATTGTTACTTCCCATGTTAA 269  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 5  
US-09-103-489-12  
Sequence 12, Application US/09103489  
Patent No. 6215048  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yennie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
STREET: 700 Chesterfield Village Parkway No. 6215048th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,489  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 286 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-103-489-12

Query Match 100.0%; Score 154; DB 3; Length 286;  
Best Local Similarity 100.0%; Pred. No. 2.9e-42;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 116 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 175  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACACTATGCTTCCC 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACACTATGCTTCCC 235  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 121 AGCTCACAATGTATTGTTACTTCCCATGTTAA 154  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 236 AGCTCACAATGTATTGTTACTTCCCATGTTAA 269  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 6  
US-09-829-381D-12  
Sequence 12, Application US/09829381D  
Patent No. 6653280  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yennie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyesum and Methods for Control  
TITLE OF INVENTION: Plant Pathogenic Fungi  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/09/829,381D  
CURRENT FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 09/103,489  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent version 3.1  
SEQ ID NO 12  
LENGTH: 286  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic PCR reaction product  
US-09-829-381D-12

Query Match 100.0%; Score 154; DB 4; Length 286;  
Best Local Similarity 100.0%; Pred. No. 2.9e-42;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 116 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 175  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACACTATGCTTCCC 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACACTATGCTTCCC 235  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 121 AGCTCACAATGTATTGTTACTTCCCATGTTAA 154  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 236 AGCTCACAATGTATTGTTACTTCCCATGTTAA 269  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 7  
US-08-627-706-9  
Sequence 9, Application US/08627706  
Patent No. 5773696  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yennie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
/ STREET: 700 Chesterfield Village Parkway No. 5773696th
/ CITY: St. Louis
/ STATE: Missouri
/ COUNTRY: USA
/ ZIP: 63198
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/627,706
/ FILING DATE:
/ CLASSIFICATION: 436
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cohen, Charles E.
/ REGISTRATION NUMBER: 34,565
/ REFERENCE/DOCKET NUMBER: 38-21 (10700) A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314) 537-6224
/ TELEFAX: (314) 537-6047
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 500 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-627-706-9

Query Match          91.0%; Score 140.2; DB 1; Length 500;
Best Local Similarity 94.8%; Pred. No. 1.4e-37;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGACATGTCAGAGTTTGTGGGAACAACATGTCATGC 61
Db 159 AAGTTGTGCGAGAGTCCAAAGTGGACATGTCAGGCGTGTGGGAATAATAACGCATGC 218
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCAACTATGCTTCCCA 121
Db 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCAACTATGCTTCCCA 278
QY 122 GCTCAAAATGTTTGTACTTCCCATGTTAA 154
Db 279 GCTCAAAATGTTTGTACTTCCCATGTTAA 311

RESULT 8
US-09-103-489-9
; Sequence 9, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/103,489
/ FILING DATE: 24-JUN-1998
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cohen, Charles E.
/ REGISTRATION NUMBER: 34,565
/ REFERENCE/DOCKET NUMBER: 38-21 (10700) A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314) 537-6224
/ TELEFAX: (314) 537-6047
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 500 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-09-103-489-9

Query Match          91.0%; Score 140.2; DB 3; Length 500;
Best Local Similarity 94.8%; Pred. No. 1.4e-37;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGACATGTCAGAGTTTGTGGGAACAACATGTCATGC 61
Db 159 AAGTTGTGCGAGAGTCCAAAGTGGACATGTCAGGCGTGTGGGAATAATAACGCATGC 218
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCAACTATGCTTCCCA 121
Db 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCAACTATGCTTCCCA 278
QY 122 GCTCAAAATGTTTGTACTTCCCATGTTAA 154
Db 279 GCTCAAAATGTTTGTACTTCCCATGTTAA 311

RESULT 9
US-09-829-381D-9
; Sequence 9, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAFF from Alysaum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Alysaum spp
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: N = any nucleotide
/ US-09-829-381D-9

Query Match          91.0%; Score 140.2; DB 4; Length 500;
Best Local Similarity 94.8%; Pred. No. 1.4e-37;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGACATGTCAGAGTTTGTGGGAACAACATGTCATGC 61
Db 159 AAGTTGTGCGAGAGTCCAAAGTGGACATGTCAGGCGTGTGGGAATAATAACGCATGC 218
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QY 62 AGGAACCAATGCAGAAACCTTTGAAGAGCAGACACGCGATCTTGCAACTATGTCTTCCCA 121  
Db 219 AGGAACCAATGCAGAAACCTTTGAAGAGCAGACACGCGATCTTGCAACTATGTCTTCCCA 278  
QY 122 GCTCACAAATGTTATTTGTTACTTCCCATGTTAA 154  
Db 279 GCTCACAAATGTTATTTGTTACTTCCCATGTTAA 311

## RESULT 10

US-08-377-687-48  
; Sequence 48, Application US/08377687  
; Patent No. 5538525  
; GENERAL INFORMATION:  
; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, FRANKY R.G.  
; APPLICANT: VANDERLEIDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/377,687  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,480  
; FILING DATE: 04-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SER.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 414 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 16..255  
US-08-377-687-48

Query Match 76.5%; Score 117.8; DB 1; Length 414;  
Best Local Similarity 85.6%; Pred. No. 4.2e-30;  
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 2 AGGTTGTCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAAACAACAATGCCATGC 61  
Db 106 AAGTTGTCGGAAGCCCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 165  
QY 62 AGGAACCAATGCAGAAACCTTTGAAGAGCAGACACGCGATCTTGCAACTATGTCTTCCCA 121  
Db 166 AAGAATCAGTGCATTAACTTTGAGAAACACGACATGGATCTTGCAACTATGTCTTCCCA 225  
QY 122 GCTCACAAATGTTATTTGTTACTTCCCATGTTAA 154

Db 226 GCTCACAAAGTATCTGCTACTTTCCTTGTTAA 258

## RESULT 11

US-08-777-192-48  
; Sequence 48, Application US/08777192  
; Patent No. 5824869  
; GENERAL INFORMATION:  
; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, FRANKY R.G.  
; APPLICANT: VANDERLEIDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,192  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,480  
; FILING DATE: 04-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SER.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 414 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 16..255  
US-08-777-192-48

Query Match 76.5%; Score 117.8; DB 1; Length 414;  
Best Local Similarity 85.6%; Pred. No. 4.2e-30;  
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 2 AGGTTGTCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAAACAACAATGCCATGC 61  
Db 106 AAGTTGTCGGAAGCCCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 165  
QY 62 AGGAACCAATGCAGAAACCTTTGAAGAGCAGACACGCGATCTTGCAACTATGTCTTCCCA 121  
Db 166 AAGAATCAGTGCATTAACTTTGAGAAACACGACATGGATCTTGCAACTATGTCTTCCCA 225  
QY 122 GCTCACAAATGTTATTTGTTACTTCCCATGTTAA 154  
Db 226 GCTCACAAAGTATCTGCTACTTTCCTTGTTAA 258

## RESULT 12

US-08-971-982-48  
; Sequence 48, Application US/08971982  
; Patent No. 6187904  
; GENERAL INFORMATION:  
; APPLICANT: BROEKAERT, WILLEM F.  
; CAMMUE, BRUNO P.A.  
; OSBORN, RUPERT W.  
; REES, SARAH B.  
; TERRAS, FRANKY R.G.  
; VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/971.982  
; FILING DATE: 17-Nov. 6187904-1997  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,480  
; FILING DATE: 04-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 414 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 16..255  
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:  
US-08-971-982-48

Query Match 76.5%; Score 117.8; DB 3; Length 414;  
Best Local Similarity 85.6%; Pred. No. 4.2e-30;  
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 2 AGTTGTGCGAGACCAAGTGGACATGTCAGGAGTTTGTGGAAACAATGCGATGC 61  
Db 106 AAGTTGTGCGAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCGATGC 165  
QY 62 AGGAACAATGCGAAGCACTTGAAGAGCAGACACCGATCTTGCACACTATGCTTCCCA 121  
Db 166 AGAATCAGTGCATTAACCTTGAAGAGCAGACATGCGATCTTGCACACTATGCTTCCCA 225  
QY 122 GCTCACAAGTATTTGTTACTTCCCATGTTAA 154  
Db 226 GCTCACAAGTATCTGCTACTTCTTGTAA 258

RESULT 13  
US-09-077-951-19  
; Sequence 19, Application US/09077951  
; Patent No. 6372888  
; GENERAL INFORMATION:

; APPLICANT: De Samblanx, Genoveva  
; APPLICANT: Broekaert, Willem  
; TITLE OF INVENTION: Antifungal Proteins  
; FILE REFERENCE: PFD50093  
; CURRENT APPLICATION NUMBER: US/09/077,951  
; CURRENT FILING DATE: 1999-03-11  
; EARLIER APPLICATION NUMBER: GB 9525474.4  
; EARLIER FILING DATE: 1995-12-13  
; EARLIER APPLICATION NUMBER: PCT/GB96/03065  
; EARLIER FILING DATE: 1996-12-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 414  
; TYPE: DNA  
; ORGANISM: Raphanus sativus  
US-09-077-951-19

Query Match 76.5%; Score 117.8; DB 4; Length 414;  
Best Local Similarity 85.6%; Pred. No. 4.2e-30;  
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 2 AGTTGTGCGAGACCAAGTGGACATGTCAGGAGTTTGTGGAAACAATGCGATGC 61  
Db 106 AAGTTGTGCGAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCGATGC 165  
QY 62 AGGAACAATGCGAAGCACTTGAAGAGCAGACACCGATCTTGCACACTATGCTTCCCA 121  
Db 166 AGAATCAGTGCATTAACCTTGAAGAGCAGACATGCGATCTTGCACACTATGCTTCCCA 225  
QY 122 GCTCACAAGTATTTGTTACTTCCCATGTTAA 154  
Db 226 GCTCACAAGTATCTGCTACTTCTTGTAA 258

RESULT 14  
US-09-077-948A-45  
; Sequence 45, Application US/09077948A  
; Patent No. 6605698  
; GENERAL INFORMATION:  
; APPLICANT: Van Amerongen, Aart  
; APPLICANT: Fant, Franky  
; APPLICANT: Borremans, Frans  
; APPLICANT: De Samblanx, Genoveva  
; APPLICANT: Sitjtsma, Lolke  
; APPLICANT: Meloen, Robbert  
; APPLICANT: Puijk, Wouter  
; APPLICANT: Schaaper, Willem  
; APPLICANT: Broekaert, Willem  
; APPLICANT: Van Gelder, Wilhelmus  
; APPLICANT: Rees, Sarah  
; TITLE OF INVENTION: Antifungal Proteins  
; FILE REFERENCE: 109846-257 (SYN-035)  
; CURRENT APPLICATION NUMBER: US/09/077,948A  
; CURRENT FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: PCT/GB96/03068  
; PRIOR FILING DATE: 1996-12-12  
; PRIOR APPLICATION NUMBER: GB 9606552.9  
; PRIOR FILING DATE: 1996-03-28  
; PRIOR APPLICATION NUMBER: GB 9525455.3  
; PRIOR FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 414  
; TYPE: DNA  
; ORGANISM: Raphanus sativus  
US-09-077-948A-45

Query Match 76.5%; Score 117.8; DB 4; Length 414;  
Best Local Similarity 85.6%; Pred. No. 4.2e-30;  
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;



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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:59:12 ; Search time 141.75 Seconds

(without alignments)  
4930.226 Million cell updates/sec

Title: US-10-681-972-12\_COPY\_116\_269

Perfect score: 154

Sequence: 1 aaggtgtgcagagaccaa.....tttgttacttcccatgtaa 154

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US05\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	270	9	US-09-829-381A-14
2	154	100.0	270	13	US-10-681-972-14
3	154	100.0	286	9	US-09-829-381A-12
4	154	100.0	286	13	US-10-681-972-12
5	140.2	91.0	500	9	US-09-829-381A-9
6	140.2	91.0	500	13	US-10-681-972-9
7	119.4	77.5	243	9	US-09-732-561-13
8	117.8	76.5	243	11	US-09-938-842A-2046
9	117.8	76.5	243	11	US-09-938-842A-2046
10	117.8	76.5	400	9	US-09-732-561-15
11	117.8	76.5	400	9	US-09-887-576-607
12	117.8	76.5	414	9	US-09-759-584-48
13	117.8	76.5	414	13	US-10-388-361A-45
14	117.8	76.5	414	14	US-10-006-252A-19

Sequence 21, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 58, Appl  
Sequence 8, Appl  
Sequence 16, Appl  
Sequence 16, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 50, Appl  
Sequence 283, Appl  
Sequence 34, Appl  
Sequence 29, Appl  
Sequence 7, Appl  
Sequence 15, Appl  
Sequence 13, Appl  
Sequence 21, Appl  
Sequence 17, Appl  
Sequence 9, Appl  
Sequence 19, Appl  
Sequence 23, Appl  
Sequence 11, Appl  
Sequence 46, Appl  
Sequence 6, Appl  
Sequence 5, Appl  
Sequence 31, Appl  
Sequence 33, Appl  
Sequence 34, Appl  
Sequence 48, Appl  
Sequence 31, Appl

15 116.2 75.5 1616 9 US-09-732-561-21  
16 115.4 74.9 308 9 US-09-829-381A-5  
17 115.4 74.9 308 13 US-10-681-972-5  
18 113 73.4 288 9 US-09-759-584-58  
19 110.6 71.8 306 9 US-09-829-381A-8  
20 110.6 71.8 306 13 US-10-681-972-8  
21 109.2 70.9 285 9 US-09-829-381A-16  
22 109.2 70.9 285 13 US-10-681-972-16  
23 102.8 66.8 285 9 US-09-829-381A-17  
24 102.8 66.8 285 13 US-10-681-972-17  
25 75.8 49.2 284 9 US-09-759-584-50  
26 54.8 35.6 373 9 US-09-770-696-283  
27 43.6 28.3 156 15 US-10-178-449A-34  
28 43.6 28.3 610 15 US-10-178-449A-29  
29 43.6 28.3 658 15 US-10-178-449A-7  
30 42.6 27.7 457 15 US-10-178-449A-15  
31 42.6 27.7 457 15 US-10-178-449A-13  
32 42.6 27.7 460 15 US-10-178-449A-21  
33 42.6 27.7 460 15 US-10-178-449A-17  
34 42.6 27.7 463 15 US-10-178-449A-9  
35 42.6 27.7 464 15 US-10-178-449A-19  
36 42.6 27.7 472 15 US-10-178-449A-23  
37 42.6 27.7 603 15 US-10-178-449A-11  
38 42.4 27.5 565 12 US-10-178-449A-46  
39 42.4 26.1 501 15 US-10-636-396-6  
40 40.2 26.1 501 15 US-10-178-449A-5  
41 39.8 25.8 150 9 US-09-759-584-31  
42 39.8 25.8 150 9 US-09-759-584-33  
43 39.8 25.8 150 9 US-09-759-584-34  
44 39 25.3 529 15 US-10-178-449A-48  
45 39 25.3 579 15 US-10-178-449A-31

#### ALIGNMENTS

#### RESULT 1

US-09-829-381A-14  
Sequence 14, Application US/09829381A  
Patent No. US20020144306A1

GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
Shah, Dilip M.  
Wu, Yonnie S.

ROSENBERGER, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

STREET: 700 Chesterfield Village Parkway No. US20020144306A1th

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/829,381A

FILING DATE: 09-Apr-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224

TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-829-381A-14

Query Match 100.0%; Score 154; DB 9; Length 270;  
Best Local Similarity 100.0%; Pred. No. 2.3e-42;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGATTTGTGGGAACAACAATGCATG 60  
DB 108 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGATTTGTGGGAACAACAATGCATG 167  
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGAACACTATGCTTCCC 120  
DB 168 CAGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGAACACTATGCTTCCC 227  
QY 121 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 154  
DB 228 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 261

## RESULT 2

US-10-681-972-14  
Sequence 14, Application US/10681972  
Publication No. US20040064850A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control  
TITLE OF INVENTION: Plant Pathogenic Fungi  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/10/681,972  
CURRENT FILING DATE: 2003-10-09  
PRIOR APPLICATION NUMBER: US/09/829,381D  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 09/103,489  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 14  
LENGTH: 270  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Plasmid  
US-10-681-972-14

Query Match 100.0%; Score 154; DB 13; Length 270;  
Best Local Similarity 100.0%; Pred. No. 2.3e-42;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGATTTGTGGGAACAACAATGCATG 60  
DB 108 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGATTTGTGGGAACAACAATGCATG 167  
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGAACACTATGCTTCCC 120  
DB 168 CAGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGAACACTATGCTTCCC 227  
QY 121 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 154  
DB 228 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 261

## RESULT 3

US-09-829-381A-12  
Sequence 12, Application US/09829381A  
Patent No. US20020144306A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Charles E. Cohen, Monsanto Company, B84F  
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/829,381A  
FILING DATE: 09-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/103,489  
FILING DATE: 1998-06-24  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 286 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-829-381A-12

Query Match 100.0%; Score 154; DB 9; Length 286;  
Best Local Similarity 100.0%; Pred. No. 2.4e-42;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGATTTGTGGGAACAACAATGCATG 60  
DB 116 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGATTTGTGGGAACAACAATGCATG 175  
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGAACACTATGCTTCCC 120  
DB 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGAACACTATGCTTCCC 235  
QY 121 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 154  
DB 236 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 269

## RESULT 4

US-10-681-972-12  
Sequence 12, Application US/10681972  
Publication No. US20040064850A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.

APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Controlling Plant Pathogenic Fungi  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/10/681,972  
CURRENT FILING DATE: 2003-10-09  
PRIOR APPLICATION NUMBER: US/09/829,381D  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 09/103,489  
PRIOR FILING DATE: 1998-06-24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 286  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic PCR reaction product  
US-10-681-972-12

Query Match 100.0%; Score 154; DB 13; Length 286;  
Best Local Similarity 100.0%; Pred. No. 2.4e-42;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAAACAACATGCATG 60  
DB 116 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAAACAACATGCATG 175

QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCAACTATGCTTTCCC 120  
DB 176 CAGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCAACTATGCTTTCCC 235

QY 121 AGCTCAAAATGTTTGTACTTCCCATGTTAA 154  
DB 236 AGCTCAAAATGTTTGTACTTCCCATGTTAA 269

RESULT 5  
US-09-829-381A-9  
Sequence 9, Application US/09829381A  
Patent No. US20020144306A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
Shah, Dilip M.  
Wu, Yonnie S.  
Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/829,381A  
FILING DATE: 09-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/103,489  
FILING DATE: 1998-06-24  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 500 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-829-381A-9

Query Match 91.0%; Score 140.2; DB 9; Length 500;  
Best Local Similarity 94.8%; Pred. No. 1.6e-37;  
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGTTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAAACAACATGCATGC 61  
DB 159 AAGTTTGTGCGAGAGTCCAAGTGGAAACATGTCAGGCGTGTGTGGGAATAATAACGCATGC 218

QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCAACTATGCTTTCCCA 121  
DB 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCAACTATGCTTTCCCA 278

QY 122 GCTCACAAATGTTTGTACTTCCCATGTTAA 154  
DB 279 GCTCACAAATGTTTGTACTTCCCATGTTAA 311

RESULT 6  
US-10-681-972-9  
Sequence 9, Application US/10681972  
Publication No. US20040064850A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Controlling Plant Pathogenic Fungi  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/10/681,972  
CURRENT FILING DATE: 2003-10-09  
PRIOR APPLICATION NUMBER: US/09/829,381D  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 09/103,489  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 500  
TYPE: DNA  
ORGANISM: Alyssum spp  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (22)-(22)  
OTHER INFORMATION: N = any nucleotide  
US-10-681-972-9

Query Match 91.0%; Score 140.2; DB 13; Length 500;  
Best Local Similarity 94.8%; Pred. No. 1.6e-37;  
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGTTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAAACAACATGCATGC 61  
DB 159 AAGTTTGTGCGAGAGTCCAAGTGGAAACATGTCAGGCGTGTGTGGGAATAATAACGCATGC 218

QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCAACTATGCTTTCCCA 121  
DB 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCAACTATGCTTTCCCA 278

QY 122 GCTCACAAATGTTTGTACTTCCCATGTTAA 154



Db 279 GCTCAAAATGATTTGTTACTTCCCATGTTAA 311

## RESULT 7

US-09-732-561-13

; Sequence 13, Application US/09732561

; Patent No. US20020035738A1

; GENERAL INFORMATION:

; APPLICANT: Thomas, Bart

; APPLICANT: Terras, Franky

; APPLICANT: Penninckx, Iris

; APPLICANT: Manners, John

; APPLICANT: Kazan, Kemal

; APPLICANT: Broekaert, Willem

; TITLE OF INVENTION: Plant Protection Method

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSER: ZENECA Ag Products

; STREET: 1800 Concord Pike

; CITY: Wilmington

; STATE: DE

; COUNTRY: USA

; ZIP: 19850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/732,561

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/202,638

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB97/01672

; FILING DATE: 20-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hohenschutz, Liza D.

; REGISTRATION NUMBER: 33,712

; REFERENCE/DOCKET NUMBER: PPD 50165/UST

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 886-1699

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 403 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; STRAIN: PDF 1.1

; US-09-732-561-13

Query Match

Best Local Similarity 77.5%; Score 119.4; DB 9; Length 403;

Matches 132; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACATGTCATGC 61

Db 116 AAGTTGTGCGAGAGCGCAAGTGGGACATGTCGCGAGTTTGGGAAACAAGTAACGCGTGC 175

QY 62 AGGAACCAATGAGAACTTGAAGAGAGACACGATCTTGAACATCTCTTCCCA 121

Db 176 AGAATCATGTCATTAACCTTGAAGAAGCAGACATGTCATCTTCCCA 235

QY 122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154

Db 236 GCTCAAAATGATCTGCTACTTCCCATGTTAA 268

## RESULT 8

US-09-938-842A-2046

; Sequence 2046, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SCRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 2046

; LENGTH: 243

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; US-09-938-842A-2046

Query Match

Best Local Similarity 76.5%; Score 117.8; DB 11; Length 243;

Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

US-09-938-842A-2046

; Sequence 2046, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SCRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 2046

; LENGTH: 243

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; US-09-938-842A-2046

Query Match

Best Local Similarity 76.5%; Score 117.8; DB 9; Length 243;

Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACATGTCATGC 61

Db 91 AAGTTGTGCGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAAGTAATGTCATGC 150

QY 62 AGGAACCAATGAGAAACCTTGAAGAGACAGACACGATCTTGAACATCTCTTCCCA 121

Db 151 AGAATCATGTCATTAACCTTGAAGAGACCAACATGTCATCTCTTCCCA 210

QY 122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154

Db 211 GCACAAAGTGTATCTGTACGTCCTCATGTTAA 243

## RESULT 9

US-09-938-842A-2046

; Sequence 2046, Application US/09938842A

; Publication No. US20040009476A9

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SCRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 2046

; LENGTH: 243

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; US-09-938-842A-2046

Query Match

Best Local Similarity 76.5%; Score 117.8; DB 11; Length 243;

Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGCATGC 61  
Db 91 AGTTTGTGCGAGAGCCAGTGGACATGTCAGGGGTTTCCGGAACAGTAATGCATGC 150  
QY 62 AGGAACCAATGCAGAAACCTTTGAAGAGCAGAACACCGATCTTCCAACTATGTTCCCA 121  
Db 151 AAGAATCAGTGCATTAACCTTTGAAGAGCAGAACACATGGATCATGCAACTATGTTCCCA 210  
QY 122 GCTCACAAATGATTTGTTACTTCCCATGTTAA 154  
Db 211 GCACACAAGTGTATCTGTACGTCCTCCATGTTAA 243

## RESULT 10

US-09-732-561-15  
; Sequence 15, Application US/09732561  
; Patent No. US20020035738A1  
; GENERAL INFORMATION:  
; APPLICANT: Thoma, Bart  
; APPLICANT: Terras, Franky  
; APPLICANT: Penninckx, Iris  
; APPLICANT: Manners, John  
; APPLICANT: Kazan, Kemal  
; APPLICANT: Broekaert, Willem  
; TITLE OF INVENTION: Plant Protection Method  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZENECA Ag Products  
; STREET: 1800 Concord Pike  
; CITY: Wilmington  
; STATE: DE  
; COUNTRY: USA  
; ZIP: 19850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/732,561  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/202,638  
; FILING DATE:  
; PRIOR APPLICATION DATA: PCT/GB97/01672  
; APPLICATION NUMBER:  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hohenschutz, Liza D.  
; REGISTRATION NUMBER: 33,712  
; REFERENCE/DOCKET NUMBER: PPD 50165/UST  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (302) 886-1699  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 400 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; STRAIN: PDF1.2

## US-09-732-561-15

Query Match 76.5%; Score 117.8; DB 9; Length 400;  
Best Local Similarity 85.6%; Pred. No. 6.5e-30;  
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 2 AGGTTGTGCGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGCATGC 61  
Db 122 AGTTTGTGCGAGAGCCAGTGGACATGTCAGGGGTTTCCGGAACAGTAATGCATGC 181

QY 62 AGGAACCAATGCAGAAACCTTTGAAGAGCAGAACACCGATCTTCCAACTATGTTCCCA 121  
Db 182 AAGAATCAGTGCATTAACCTTTGAAGAGCAGAACACATGGATCATGCAACTATGTTCCCA 241  
QY 122 GCTCACAAATGATTTGTTACTTCCCATGTTAA 154  
Db 242 GCACACAAGTGTATCTGTAGTCCCATGTTAA 274

## RESULT 11

US-09-887-576-607  
; Sequence 607, Application US/09887576  
; Patent No. US2002014047A1  
; GENERAL INFORMATION:  
; APPLICANT: Bugworth, P.  
; APPLICANT: Brown, D.  
; APPLICANT: Chang, H.  
; APPLICANT: Zhu, T.  
; APPLICANT: Han, B.  
; APPLICANT: Wang, X.  
; APPLICANT: Cooper, Bret  
; TITLE OF INVENTION: Promoters for regulation of plant expression  
; FILE REFERENCE: 1360.001US1  
; CURRENT APPLICATION NUMBER: US/09/887,576  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: US 60/213,848  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/214,087  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/258,692  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 875  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 607  
; LENGTH: 400  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(400)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-887-576-607

Query Match 76.5%; Score 117.8; DB 9; Length 400;  
Best Local Similarity 85.6%; Pred. No. 6.5e-30;  
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGCATGC 61  
Db 122 AGTTTGTGCGAGAGCCAGTGGACATGTCAGGGGTTTCCGGAACAGTAATGCATGC 181  
QY 62 AGGAACCAATGCAGAAACCTTTGAAGAGCAGAACACCGATCTTCCAACTATGTTCCCA 121  
Db 182 AAGAATCAGTGCATTAACCTTTGAAGAGCAGAACACATGGATCATGCAACTATGTTCCCA 241  
QY 122 GCTCACAAATGATTTGTTACTTCCCATGTTAA 154  
Db 242 GCACACAAGTGTATCTGTAGTCCCATGTTAA 274

## RESULT 12

US-09-759-584-48  
; Sequence 48, Application US/09759584  
; Patent No. US20010014732A1  
; GENERAL INFORMATION:  
; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, FRANKY R.G.  
; APPLICANT: VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS

NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/759,584  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/377,687  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 16..255  
US-09-759-584-48

Query Match 76.5%; Score 117.8; DB 9; Length 414;  
Best Local Similarity 85.6%; Pred. No. 6.6e-30;  
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 2 AGGTTGTGCGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACATGCGATGC 61  
Db 106 AAGTTGTGCGAAGGCCAAGTGGGACATGCTCAGGAGTCTGTGGAACAATAACGCGATGC 165  
QY 62 AGGAACCAATGCGAAGACCTTGAAGAGCAGACACGGATCTTGCACATATGCTTTCCCA 121  
Db 166 AGAATCAGTGCATTAACTTGAAGAACGACGACATGGATCTTGGCAACTATGCTTTCCCA 225  
QY 122 GCTCACAATGATTTGTTACTTCCCATGTTAA 154  
Db 226 GCTCACAAGTATCTGCTACTTCTCTGTTAA 258

RESULT 13  
US-10-388-361A-45  
Sequence 45, Application US/10388361A  
Publication No. US20030226169A1  
GENERAL INFORMATION:  
APPLICANT: Van Amerongen, Aart  
APPLICANT: Fant, Franky  
APPLICANT: Borremans, Frans  
APPLICANT: De Samblanx, Genoveva  
APPLICANT: Sitjtsma, Lolke  
APPLICANT: Melen, Robbert  
APPLICANT: Fuijk, Wouter  
APPLICANT: Schaaper, Wilhelms  
APPLICANT: Broekaert, Willem  
APPLICANT: Van Gelder, Wilhelms  
APPLICANT: Rees, Sarah  
TITLE OF INVENTION: Antifungal Proteins

FILE REFERENCE: 50094PPDDIV  
CURRENT APPLICATION NUMBER: US/10/388,361A  
CURRENT FILING DATE: 2003-03-13  
PRIOR APPLICATION NUMBER: US 09/077,948  
PRIOR FILING DATE: 1998-08-07  
PRIOR APPLICATION NUMBER: PCT/GB96/03068  
PRIOR FILING DATE: 1996-12-12  
PRIOR APPLICATION NUMBER: GB 9606552.9  
PRIOR FILING DATE: 1996-03-28  
PRIOR APPLICATION NUMBER: GB 9525455.3  
PRIOR FILING DATE: 1995-12-13  
NUMBER OF SEQ ID NOS: 141  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 45  
LENGTH: 414  
TYPE: DNA  
ORGANISM: Raphanus sativus  
US-10-388-361A-45

Query Match 76.5%; Score 117.8; DB 13; Length 414;  
Best Local Similarity 85.6%; Pred. No. 6.6e-30;  
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 2 AGGTTGTGCGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACATGCGATGC 61  
Db 106 AAGTTGTGCGAAGGCCAAGTGGGACATGCTCAGGAGTCTGTGGAACAATAACGCGATGC 165  
QY 62 AGGAACCAATGCGAAGACCTTGAAGAGCAGACACGGATCTTGCACATATGCTTTCCCA 121  
Db 166 AGAATCAGTGCATTAACTTGAAGAACGACGACATGGATCTTGGCAACTATGCTTTCCCA 225  
QY 122 GCTCACAATGATTTGTTACTTCCCATGTTAA 154  
Db 226 GCTCACAAGTATCTGCTACTTCTCTGTTAA 258

RESULT 14  
US-10-006-252A-19  
Sequence 13, Application US/10006252A  
Publication No. US20020152498A1  
GENERAL INFORMATION:  
APPLICANT: De Samblanx, Genoveva  
APPLICANT: Broekaert, Willem  
APPLICANT: Rees, Sarah  
TITLE OF INVENTION: Antifungal Proteins  
FILE REFERENCE: SYN-034DV  
CURRENT APPLICATION NUMBER: US/10/006,252A  
CURRENT FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 09/077,951  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: GB 9525474.4  
PRIOR FILING DATE: 1995-12-13  
PRIOR APPLICATION NUMBER: PCT/GB96/03065  
PRIOR FILING DATE: 1996-12-12  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 414  
TYPE: DNA  
ORGANISM: Raphanus sativus  
US-10-006-252A-19

Query Match 76.5%; Score 117.8; DB 14; Length 414;  
Best Local Similarity 85.6%; Pred. No. 6.6e-30;  
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 2 AGGTTGTGCGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACATGCGATGC 61  
Db 106 AAGTTGTGCGAAGGCCAAGTGGGACATGCTCAGGAGTCTGTGGAACAATAACGCGATGC 165  
QY 62 AGGAACCAATGCGAAGACCTTGAAGAGCAGACACGGATCTTGCACATATGCTTTCCCA 121  
Db 166 AGAATCAGTGCATTAACTTGAAGAACGACGACATGGATCTTGGCAACTATGCTTTCCCA 225

Db 1535 GCACACAAGTGATCTGTACGTCCCATGTAA 1567

Search completed: May 18, 2004, 20:33:21  
Job time : 141.75 secsQY 122 GCTCACAAATGATTTGTTACTTCCCATGTAA 154  
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Db 226 GCTCACAAAGTGATCTGTACTTCCCTGTAA 258  
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## RESULT 15

US-09-732-561-21  
; Sequence 21, Application US/09732561  
; Patent No. US20020035738A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomma, Bart  
; APPLICANT: Terras, Franky  
; APPLICANT: Penninckx, Iris  
; APPLICANT: Manners, John  
; APPLICANT: Kazan, Kemal  
; APPLICANT: Broekaert, Willem  
; TITLE OF INVENTION: Plant Protection Method  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZENECA Ag Products  
; STREET: 1800 Concord Pike  
; CITY: Wilmington  
; STATE: DE  
; COUNTRY: USA  
; ZIP: 19850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/732,561  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/202,638  
; FILING DATE:  
; PRIOR APPLICATION DATA: PCT/GB97/01672  
; APPLICATION NUMBER: 20-JUN-1997  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hohenschutz, Liza D.  
; REGISTRATION NUMBER: 33,712  
; REFERENCE/DOCKET NUMBER: PPD 50165/UST  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (302) 886-1699  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1616 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; STRAIN: Arabidopsis PDF1.2 gene  
; INDIVIDUAL ISOLATE: DNA sequence Figure 14  
US-09-732-561-21

Query Match 75.5%; Score 116.2; DB 9; Length 1616;  
Best Local Similarity 85.0%; Pred.No. 4.1e-29;  
Matches 130; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
QY 2 AGGTGTGGCAGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGCATGC 61  
|||||  
Db 1415 AGTTGTCCGAGAGCCCAAGTGGACATGTCAGGGTTTGCAGAACACATATGCATGC 1474  
|||||  
QY 62 AGGAACCAATGCGAAGAACCTTGAAGACGACGATCTTGCACACTATGTCTTCCCA 121  
|||||  
Db 1475 AAGAATCAGTGCATTAACTCTGAAGAGCCCAACATGATCATGCACACTATGTCTTCCCA 1534  
|||||  
QY 122 GCTCACAAATGATTTGTTACTTCCCATGTAA 154  
|||||

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:15:17 ; Search time 1680 Seconds  
(without alignments)  
3225.394 Million cell updates/sec

Title: US-10-681-972-12\_COPY\_116\_269

Perfect score: 154

Sequence: 1 aaggtgtgcagagaccaa.....ttgttacttcccatgtaa 154

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 37577330 segs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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103: /cgn2\_6/ptodata/2/pna/US6046\_COMB.seq:  
104: /cgn2\_6/ptodata/2/pna/US6047\_COMB.seq:  
105: /cgn2\_6/ptodata/2/pna/US6048\_COMB.seq:  
106: /cgn2\_6/ptodata/2/pna/US6049\_COMB.seq:  
107: /cgn2\_6/ptodata/2/pna/US6050\_COMB.seq:  
108: /cgn2\_6/ptodata/2/pna/US6051\_COMB.seq:  
109: /cgn2\_6/ptodata/2/pna/US6052\_COMB.seq:  
110: /cgn2\_6/ptodata/2/pna/US6053\_COMB.seq:

Result No.	Score	Query Match	Length	DB ID	Description
1	154	100.0	270	53	US-10-681-972-14
2	154	100.0	286	53	US-10-681-972-12
3	140.2	91.0	500	53	US-10-681-972-9
4	122.6	79.6	243	30	US-09-708-427-18199
5	122.6	79.6	243	38	US-09-935-625-5250
6	122.6	79.6	243	38	US-09-935-625-5383
7	122.6	79.6	243	38	US-09-935-625-28557
8	122.6	79.6	243	38	US-09-935-625-28943
9	122.6	79.6	584	21	US-09-505-533-7439
10	122.6	79.6	584	33	US-09-819-091A-7439
11	122.6	79.6	61290	22	US-09-534-853-830
12	122.6	79.6	61290	33	US-09-803-736-830
13	122.6	79.6	87080	22	US-09-534-853-284
14	122.6	79.6	87080	33	US-09-803-736-284
15	119.4	77.5	243	30	US-09-708-427-21472
16	119.4	77.5	243	36	US-09-887-272A-747
17	119.4	77.5	243	38	US-09-935-625-5372
18	119.4	77.5	243	38	US-09-935-625-28904
19	119.4	77.5	243	50	US-10-380-710-170
20	119.4	77.5	243	50	US-10-380-710-365
21	119.4	77.5	403	16	US-09-202-638-13
22	119.4	77.5	403	31	US-09-732-561-13
23	119.4	77.5	418	27	US-09-654-617-117133
24	119.4	77.5	418	29	US-09-684-016-117133
25	119.4	77.5	595	21	US-09-505-533-7438
26	119.4	77.5	595	33	US-09-819-091A-7438
27	119.4	77.5	97208	22	US-09-534-853-136
28	119.4	77.5	97208	33	US-09-803-736-136
29	117.8	76.5	243	38	US-09-938-842A-2046
30	117.8	76.5	243	50	US-10-380-710-93
31	117.8	76.5	243	50	US-10-380-710-266
32	117.8	76.5	243	95	US-60-382-898-1141
33	117.8	76.5	243	95	US-60-382-898-1150
34	117.8	76.5	400	16	US-09-202-638-15
35	117.8	76.5	400	31	US-09-732-561-15
36	117.8	76.5	400	36	US-09-887-576-607
37	117.8	76.5	400	46	US-10-177-253-215
38	117.8	76.5	414	5	US-08-178-430-37
39	117.8	76.5	414	8	US-08-452-078-48
40	117.8	76.5	414	31	US-09-759-584-48
41	117.8	76.5	414	43	US-10-006-252A-19
42	117.8	76.5	414	50	US-10-388-361A-45
43	117.8	76.5	439	74	US-60-184-698-919
44	117.8	76.5	715	27	US-09-654-617-132225
45	117.8	76.5	715	29	US-09-684-016-132225

## ALIGNMENTS

RESULT 1  
US-10-681-972-14  
; Sequence 14, Application US/10681972  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yennie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control  
; FILE REFERENCE: 38-21 (10700) C  
; CURRENT FILING DATE: 2003-10-09  
; PRIOR APPLICATION NUMBER: US/09/829,381D  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/103,489  
; PRIOR FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in version 3.1

; SEQ ID NO 14  
; LENGTH: 270  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid  
US-10-681-972-14  
  
Query Match 100.0%; Score 154; DB 53; Length 270;  
Best Local Similarity 100.0%; Pred. No. 7.1e-39;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAACAATGCATG 60  
Db 108 AGTTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAACAATGCATG 167  
  
QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGACAGAACACCGATCTTGCACATATGTCTTCCC 120  
Db 168 CAGGAACCAATGCAGAAACCTTGAAGAGACAGAACACCGATCTTGCACATATGTCTTCCC 227  
  
QY 121 AGCTCACAATGTATTGTACTTCCCATGTTAA 154  
Db 228 AGCTCACAATGTATTGTACTTCCCATGTTAA 261  
  
RESULT 2  
US-10-681-972-12  
; Sequence 12, Application US/10681972  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yennie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control  
; FILE REFERENCE: 38-21 (10700) C  
; CURRENT FILING DATE: 2003-10-09  
; PRIOR APPLICATION NUMBER: US/09/829,381D  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/103,489  
; PRIOR FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 12  
; LENGTH: 286  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic PCR reaction product  
US-10-681-972-12  
  
Query Match 100.0%; Score 154; DB 53; Length 286;  
Best Local Similarity 100.0%; Pred. No. 7.3e-39;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAACAATGCATG 60  
Db 116 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAACAATGCATG 175  
  
QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGACAGAACACCGATCTTGCACATATGTCTTCCC 120  
Db 176 CAGGAACCAATGCAGAAACCTTGAAGAGACAGAACACCGATCTTGCACATATGTCTTCCC 235  
  
QY 121 AGCTCACAATGTATTGTACTTCCCATGTTAA 154  
Db 236 AGCTCACAATGTATTGTACTTCCCATGTTAA 269  
  
RESULT 3  
US-10-681-972-9  
; Sequence 9, Application US/10681972  
; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong  
 ; APPLICANT: Shah, Dilip M.  
 ; APPLICANT: Wu, Yonnie S.  
 ; APPLICANT: Rosenberger, Cindy A.  
 ; TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyesum and Methods for Control  
 ; FILE REFERENCE: 38-21 (10700) C  
 ; CURRENT APPLICATION NUMBER: US/10/681,972  
 ; CURRENT FILING DATE: 2003-10-09  
 ; PRIOR APPLICATION NUMBER: US/09/829,381D  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: 09/103,489  
 ; PRIOR FILING DATE: 1998-06-24  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 9  
 ; LENGTH: 500  
 ; TYPE: DNA  
 ; ORGANISM: Alyesum spp  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (22)-(22)  
 ; OTHER INFORMATION: N = any nucleotide  
 US-10-681-972-9

Query Match 91.0%; Score 140.2; DB 53; Length 500;  
 Best Local Similarity 94.8%; Pred. No. 2.5e-34;  
 Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGAGTTGTGGGAAACAATGCAATGC 61  
 DB 159 AAGTTGTGCGAGAGTCCAAAGTGGAAACATGTCAGGCGTGTGGGAAATAAAGCCATGC 218  
 QY 62 AGGAACCAATCGAACAACCTTGAAGAGCAGACACGATCTTCAACTATGTTCTTCCCA 121  
 DB 219 AGGAACCAATCGAACAACCTTGAAGAGCAGACACGATCTTCAACTATGTTCTTCCCA 278  
 QY 122 GCTCACAATGTAATTTGTTACTTCCCATGTTAA 154  
 DB 279 GCTCACAATGTAATTTGTTACTTCCCATGTTAA 311

RESULT 4  
 US-09-708-427-18199  
 ; Sequence 18199, Application US/09708427  
 ; GENERAL INFORMATION:  
 ; APPLICANT: N. ALEXANDROV et al.  
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
 ; FILE REFERENCE: 2750-1243P  
 ; CURRENT APPLICATION NUMBER: US/09/708,427  
 ; CURRENT FILING DATE: 2000-11-09  
 ; NUMBER OF SEQ ID NOS: 85364  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 18199  
 ; LENGTH: 243  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: 1..243  
 ; OTHER INFORMATION: any n = a, g, c, t, unknown, or other  
 ; NAME/KEY: misc feature  
 ; LOCATION: 1..243  
 ; OTHER INFORMATION: Ceres Seq. ID 1833757  
 US-09-708-427-18199

Query Match 79.6%; Score 122.6; DB 30; Length 243;  
 Best Local Similarity 87.6%; Pred. No. 9.8e-29;  
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
 QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGAGTTGTGGGAAACAATGCAATGC 61

Db 91 AAGTTGTGCGAGAGCCAGTGACTTGGTCAGAGTTTGGGNAACAGCAATGTCATGC 150  
 QY 62 AGGAACCAATCGAACAACCTTGAAGAGCAGACACGATCTTCAACTATGTTCTTCCCA 121  
 Db 151 AAGAATCAGTGCATTAACCTTGAAGAGGAGCAAAACATGATCTTGCAACTATGTTCTTCCCA 210  
 QY 122 GCTCACAATGTAATTTGTTACTTCCCATGTTAA 154  
 Db 211 GCTCACAAGTATCTGTTACGTCCCATGTTAA 243

RESULT 5  
 US-09-935-625-5250  
 ; Sequence 5250, Application US/09935625  
 ; GENERAL INFORMATION:  
 ; APPLICANT: N. ALEXANDROV et al.  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE  
 ; FILE REFERENCE: 2750-1481P  
 ; CURRENT APPLICATION NUMBER: US/09/935,625  
 ; CURRENT FILING DATE: 2001-08-24  
 ; NUMBER OF SEQ ID NOS: 33136  
 ; SEQ ID NO 5250  
 ; LENGTH: 243  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: Misc feature  
 ; LOCATION: 1..243  
 ; OTHER INFORMATION: Ceres Seq. ID no. 2143607  
 US-09-935-625-5250

Query Match 79.6%; Score 122.6; DB 38; Length 243;  
 Best Local Similarity 87.6%; Pred. No. 9.8e-29;  
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
 QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGAGTTTGGGAAACAACATGCAATGC 61  
 Db 91 AAGTTGTGCGAGAGCCAGTGGGACATGTCAGGCGTTTCCGGAACAGTAATGCAATGC 150  
 QY 62 AGGAACCAATCGAACAACCTTGAAGAGCAGACACGATCTTCAACTATGTTCTTCCCA 121  
 Db 151 AAGAATCAGTGCATTAACCTTGAAGAGGAGCAAAACATGATCTTGCAACTATGTTCTTCCCA 210  
 QY 122 GCTCACAATGTAATTTGTTACTTCCCATGTTAA 154  
 Db 211 GCTCACAATGTAATCTGTTACGTCCCATGTTAA 243

RESULT 6  
 US-09-935-625-5383  
 ; Sequence 5383, Application US/09935625  
 ; GENERAL INFORMATION:  
 ; APPLICANT: N. ALEXANDROV et al.  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE  
 ; FILE REFERENCE: 2750-1481P  
 ; CURRENT APPLICATION NUMBER: US/09/935,625  
 ; CURRENT FILING DATE: 2001-08-24  
 ; NUMBER OF SEQ ID NOS: 33136  
 ; SEQ ID NO 5383  
 ; LENGTH: 243  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: Misc feature  
 ; LOCATION: 1..243  
 ; OTHER INFORMATION: Ceres Seq. ID no. 2711695  
 US-09-935-625-5383

Query Match 79.6%; Score 122.6; DB 38; Length 243;  
 Best Local Similarity 87.6%; Pred. No. 9.8e-29;  
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTCTTGTGGGAACAACATGATGC 61  
Db 91 AAGTTGTGCGAGAGACCAAGTGGTACTTGTGTCAGGAGTTTGGGAACAGCAATGATGC 150  
QY 62 AGGAACCAATGCGAAGAACCTTTGAAAGAGCAGAACACCGATCTTGGCAACTATGCTTCCCA 121  
Db 151 AAGAATCAGTGCAATTACCTTTGAAGGAGCAAAACATGGATCTTGGCAACTATGCTTCCCA 210  
QY 122 GCTCACAATGATTTGTTACTTCCCATGTAA 154  
Db 211 GCTCACAATGATTTGTTACTTCCCATGTAA 243

## RESULT 7

US-09-935-625-28557  
; Sequence 28557, Application US/09935625  
; GENERAL INFORMATION:  
; APPLICANT: N. ALEXANDROV et al.  
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE  
; FILE REFERENCE: 2750-1481P  
; CURRENT APPLICATION NUMBER: US/09/935,625  
; CURRENT FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 33136  
; SEQ ID NO 28557  
; LENGTH: 243  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; NAME/KEY: Misc\_feature  
; LOCATION: 1..243  
; OTHER INFORMATION: Ceres Seq. ID no. 2143607  
US-09-935-625-28557

Query Match 79.6%; Score 122.6; DB 38; Length 243;  
Best Local Similarity 87.6%; Pred. No. 9.8e-29;  
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTCTTGTGGGAACAACATGATGC 61  
Db 91 AAGTTGTGCGAGAGACCAAGTGGTACTTGTGTCAGGAGTTTGGGAACAGCAATGATGC 150  
QY 62 AGGAACCAATGCGAAGAACCTTTGAAAGAGCAGAACACCGATCTTGGCAACTATGCTTCCCA 121  
Db 151 AAGAATCAGTGCAATTACCTTTGAAGGAGCAAAACATGGATCTTGGCAACTATGCTTCCCA 210  
QY 122 GCTCACAATGATTTGTTACTTCCCATGTAA 154  
Db 211 GCTCACAATGATTTGTTACTTCCCATGTAA 243

## RESULT 8

US-09-935-625-28943  
; Sequence 28943, Application US/09935625  
; GENERAL INFORMATION:  
; APPLICANT: N. ALEXANDROV et al.  
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE  
; FILE REFERENCE: 2750-1481P  
; CURRENT APPLICATION NUMBER: US/09/935,625  
; CURRENT FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 33136  
; SEQ ID NO 28943  
; LENGTH: 243  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; NAME/KEY: Misc\_feature  
; LOCATION: 1..243  
; OTHER INFORMATION: Ceres Seq. ID no. 2711695  
US-09-935-625-28943

Query Match 79.6%; Score 122.6; DB 38; Length 243;  
Best Local Similarity 87.6%; Pred. No. 9.8e-29;  
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTCTTGTGGGAACAACATGATGC 61  
Db 91 AAGTTGTGCGAGAGACCAAGTGGTACTTGTGTCAGGAGTTTGGGAACAGCAATGATGC 150  
QY 62 AGGAACCAATGCGAAGAACCTTTGAAAGAGCAGAACACCGATCTTGGCAACTATGCTTCCCA 121  
Db 151 AAGAATCAGTGCAATTACCTTTGAAGGAGCAAAACATGGATCTTGGCAACTATGCTTCCCA 210  
QY 122 GCTCACAATGATTTGTTACTTCCCATGTAA 154  
Db 211 GCTCACAATGATTTGTTACTTCCCATGTAA 243

## RESULT 9

US-09-505-532-7439/c  
; Sequence 7439, Application US/09505532  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15478)B  
; CURRENT APPLICATION NUMBER: US/09/505,532  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-12;  
; PRIOR FILING DATE: USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-12;  
; NUMBER OF SEQ ID NOS: 51470  
; SEQ ID NO 7439  
; LENGTH: 584  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-505-532-7439

Query Match 79.6%; Score 122.6; DB 21; Length 584;  
Best Local Similarity 87.6%; Pred. No. 1.3e-28;  
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTCTTGTGGGAACAACATGATGC 61  
Db 290 AAGTTGTGCGAGAGACCAAGTGGTACTTGTGTCAGGAGTTTGGGAACAGCAATGATGC 231  
QY 62 AGGAACCAATGCGAAGAACCTTTGAAAGAGCAGAACACCGATCTTGGCAACTATGCTTCCCA 121  
Db 230 AAGAATCAGTGCAATTACCTTTGAAGGAGCAAAACATGGATCTTGGCAACTATGCTTCCCA 171  
QY 122 GCTCACAATGATTTGTTACTTCCCATGTAA 154  
Db 170 GCTCACAATGATTTGTTACTTCCCATGTAA 138

## RESULT 10

US-09-819-091A-7439/c  
; Sequence 7439, Application US/09819091A  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15478)B  
; CURRENT APPLICATION NUMBER: US/09/819,091A  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: US 60/108,420  
; PRIOR FILING DATE: 1998-11-16  
; PRIOR APPLICATION NUMBER: US 60/120,645  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 09/443,025  
; NUMBER OF SEQ ID NOS: 51470  
; SEQ ID NO 7439  
; LENGTH: 584  
; TYPE: DNA



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; ORGANISM: Arabidopsis thaliana
US-09-819-091A-7439

Query Match
Best Local Similarity 79.6%; Score 122.6; DB 33; Length 584;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACATGCAATGC 61
Db |||||
QY 62 AGGACCAATGCGAAGACCTTGAAGAGACGACACGAGTCTTGCAACTATGCTTCCCA 121
Db |||||
QY 230 AAGTGTGCGAGAGCAAGTGGTACTTGGTCAGGAGTTTGGGAAACAGCAATGCAATGC 231
Db |||||

QY 122 GCTCACAATGTAATGTTTACTTCCCATGTTAA 154
Db |||||

RESULT 11
US-09-534-859-830/c
; Sequence 830, Application US/09534859
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Last, Robert L.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: PLANT POLYMORPHIC MARKERS AND USES THEREOF
; FILE REFERENCE: 38-10(15493)B
; CURRENT APPLICATION NUMBER: US/09/534,859
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 1127
; SEQ ID NO 830
; LENGTH: 61290
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-534-859-830

Query Match
Best Local Similarity 79.6%; Score 122.6; DB 22; Length 61290;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACATGCAATGC 61
Db |||||
QY 62 AGGACCAATGCGAAGACCTTGAAGAGACGACACGAGTCTTGCAACTATGCTTCCCA 121
Db |||||
QY 22629 AAGAATCAGTGCATTAACCTTGAAGAGACCAAAACATGGATCTTGCAACTATGCTTCCCA 22570
Db |||||

RESULT 12
US-09-803-736-830/c
; Sequence 830, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: identified by Attorney Docket number 04993.0206CPUS01 38-10,
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 830
; LENGTH: 61290
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-830

Query Match
Best Local Similarity 79.6%; Score 122.6; DB 33; Length 61290;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACATGCAATGC 61
Db |||||
QY 22689 AAGTTGTGCGAGAGCAAGTGGGACATGGTCAGGAGTTTGGGAAACAGTAAATGCAATGC 22630
Db |||||
QY 62 AGGAACCAATGCGAAGACCTTGAAGAGACGACACGAGTCTTGCAACTATGCTTCCCA 121
Db |||||
QY 22629 AAGAATCAGTGCATTAACCTTGAAGAGACCAAAACATGGATCTTGCAACTATGCTTCCCA 22570
Db |||||
QY 122 GCTCACAATGTAATGTTTACTTCCCATGTTAA 154
Db |||||
QY 22569 GCTCACAATGTAATGTTTACTTCCCATGTTAA 22537
Db |||||

RESULT 13
US-09-534-859-284/c
; Sequence 284, Application US/09534859
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Last, Robert L.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: PLANT POLYMORPHIC MARKERS AND USES THEREOF
; FILE REFERENCE: 38-10(15493)B
; CURRENT APPLICATION NUMBER: US/09/534,859
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 1127
; SEQ ID NO 284
; LENGTH: 87080
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-534-859-284

Query Match
Best Local Similarity 79.6%; Score 122.6; DB 22; Length 87080;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACATGCAATGC 61
Db |||||
QY 55050 AAGTTGTGCGAGAGCAAGTGGTACTTGGTCAGGAGTTTGGGAAACAGCAATGCAATGC 54991
Db |||||
QY 62 AGGACCAATGCGAAGACCTTGAAGAGACGACACGAGTCTTGCAACTATGCTTCCCA 121
Db |||||
QY 54990 AAGAATCAGTGCATTAACCTTGAAGAGACCAAAACATGGATCTTGCAACTATGCTTCCCA 54931
Db |||||
QY 122 GCTCACAATGTAATGTTTACTTCCCATGTTAA 154
Db |||||
QY 54930 GCTCACAATGTAATGTTTACTTCCCATGTTAA 54898
Db |||||

RESULT 14
US-09-803-736-284/c
; Sequence 284, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
```

Query Match	77.5%;	Score 119.4;	DB 30;	Length 243;
Best Local Similarity	86.3%;	Pred. No. 1.1e-27;		
Matches 132;	Conservative 0;	Mismatches 21;	Indels 0;	Gaps 0;
OY	2	AGTTGTGCGAGAGCCAAAGTGGGACATGCTCAGGAGTTTGTGGGAAACAACATGCGATGC	61	
Db	91	AAGTTGTGCGAGAGCCAAAGTGGTACTTGGTCAGGAGTTTGGGAAACCAATGGGTGC	150	
OY	62	AGGAACCAATGCAGAAACCTTGAAGAGCAGAAACACGGATCTTGCACACTATGCTTCCCA	121	
Db	151	AAGAATCAGTGCATTAACTTGGGGGGCAACATGGATCTTGCACACTATGCTTCCCA	210	
OY	122	GTCACAAATGATTGTGTTACTTCCCATTGTA	154	

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:22:46 ; Search time 67.55 Seconds  
(without alignments)  
2842.409 Million cell updates/sec

Title: US-10-681-972-12\_COPY\_116\_269

Perfect score: 154

Sequence: 1 aaggtgtgagagacaa.....ttgttacttcccatgtaa 154

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1745496 seqs, 623391994 residues

Total number of hits satisfying chosen parameters: 3490992

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA New.\*

- 1: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	35.2	22.9	163548	6	US-10-767-471-10730
C 2	34.6	22.5	42063	6	US-10-417-375A-151
C 3	34.6	22.5	42063	6	US-10-417-375B-151
4	31	20.1	201	7	US-60-568-845-22848
5	31	20.1	201	7	US-60-568-845-22851
6	31	20.1	201	7	US-60-568-845-22854
7	31	20.1	201	7	US-60-568-845-22856
8	31	20.1	201	7	US-60-568-845-22858
9	31	20.1	96902	7	US-60-568-845-22858
10	30.4	19.7	201	7	US-60-568-845-22832
11	30.4	19.7	201	7	US-60-568-845-22842
12	30.4	19.7	201	7	US-60-568-845-22842
C 13	30.4	19.7	1207	1	PCT-US03-41761-31797
C 14	30.4	19.7	1207	1	PCT-US03-41761-31797
15	30	19.5	201	7	US-60-568-845-22830
16	29.8	19.4	76053	6	US-10-767-471-10882
C 17	29.6	19.2	1490	1	PCT-US03-41761-34711
C 18	29.6	19.2	1490	1	PCT-US03-41761-34711
19	29.2	19.0	37544	5	US-09-889-874A-52
20	29	18.8	599	7	US-60-545-213-4176
21	29	18.8	599	7	US-60-545-213-4176
22	28.8	18.7	201	7	US-60-563-440-3885
23	28.8	18.7	201	7	US-60-563-440-3885
C 24	28.8	18.7	2046	1	PCT-US03-41761-48667
C 25	28.8	18.7	2046	1	PCT-US03-41761-48667
26	28.8	18.7	3254	7	US-60-563-440-196

27	28.8	18.7	15254	7	US-60-563-440-11946
C 28	28.6	18.6	35126	6	US-10-796-307-8785
29	28.6	18.6	161065	6	US-10-796-280-12265
30	28.6	18.6	161065	6	US-10-796-307-8875
C 31	28.6	18.6	1184710	6	US-10-796-280-12394
C 32	28.6	18.6	1184710	7	US-60-568-845-2921
33	28.4	18.4	201	6	US-10-767-471-25146
34	28.4	18.4	201	6	US-10-796-280-27009
35	28.4	18.4	1331	1	PCT-US04-05654-1590
36	28.4	18.4	261922	6	US-10-767-471-10653
37	28.4	18.4	261922	6	US-10-796-280-12264
C 38	28	18.2	201	7	US-60-568-219-7921
C 39	28	18.2	653	6	US-10-767-701-22795
40	28	18.2	1711	1	PCT-US03-41761-31570
41	28	18.2	1711	1	PCT-US03-41761-31570
42	28	18.2	209822	6	US-10-796-280-12169
43	28	18.2	209822	7	US-60-568-219-6144
C 44	28	18.2	380939	7	US-60-568-219-6153
C 45	27.8	18.1	1663	1	PCT-US03-41761-45120

#### ALIGNMENTS

##### RESULT 1

US-10-767-471-10730/c  
; Sequence 10730, Application US/10767471  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001505  
; CURRENT APPLICATION NUMBER: US/10/767,471  
; CURRENT FILING DATE: 2004-01-30  
; NUMBER OF SEQ ID NOS: 50231  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10730  
; LENGTH: 163548  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(163548)  
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-7)  
US-10-767-471-10730

Query Match		22.9%	Score 35.2;	DB 6;	Length 163548;
Best Local Similarity		52.8%	Pred. No. 0.28;		
Matches		76;	Conservative	0;	Mismatches 68;
				Indels	0;
				Gaps	0;
Qy	3	GGTGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAAACAACTGCGATGCA	62		
Db	157637	GGTGATCTCAAGAACTGGTGTATCAGATATCAGAAGAGAGAACTGGGAAAGATAGCA	157578		
Qy	63	GGAAACCAATCAGAAACCTTGAAGACGACAGACGATCTTGCAACTGTCTTCCAG	122		
Db	157577	GGCAATTAAGATAGACTTAGTAGGAAAATCATATTTTAAATAATCTTTTATTG	157518		
Qy	123	CTCACAATGTATTGTGTACTTC	146		
Db	157517	CTCACCATAGACATTCGACCTAC	157494		

##### RESULT 2

US-10-417-375A-151/c  
; Sequence 151, Application US/10417375A  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer  
; FILE REFERENCE: 52945201600  
; CURRENT APPLICATION NUMBER: US/10/417,375A  
; CURRENT FILING DATE: 2003-04-15

```
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 42063
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(42063)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-151

Query Match      22.5%; Score 34.6; DB 6; Length 42063;
Best Local Similarity 59.8%; Pred. No. 0.26;
Matches 58; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 AAGGTGTGCGAGAGACCAAGTGGGACATGGTACGAGTGTGGGAAACAACAAATCATG 60
Db 9183 AAGGCTCAGCTACATACCAAGGCAACCTGGTACGCGGTGTGTTCCATCAGAGGGTC 9124

QY 61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACAC 97
Db 9123 CAGGCCCTCTGCAGTCACCTGACAAACCCAGGAAC 9087

RESULT 3
US-10-417-375B-151/c
; Sequence 151, Application US/10417375B
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375B
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 42063
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(42063)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375B-151

Query Match      22.5%; Score 34.6; DB 6; Length 42063;
Best Local Similarity 59.8%; Pred. No. 0.26;
Matches 58; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 AAGGTGTGCGAGAGACCAAGTGGGACATGGTACGAGTGTGGGAAACAACAAATCATG 60
Db 9183 AAGGCTCAGCTACATACCAAGGCAACCTGGTACGCGGTGTGTTCCATCAGAGGGTC 9124

QY 61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACAC 97
Db 9123 CAGGCCCTCTGCAGTCACCTGACAAACCCAGGAAC 9087

RESULT 4
US-60-568-845-22848
; Sequence 22848, Application US/60568845
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/60/568,845
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 39608
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22848
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-568-845-22848

Query Match      20.1%; Score 31; DB 7; Length 201;
Best Local Similarity 62.0%; Pred. No. 0.51;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 53 AATGCATGCAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCACAT 112
Db 123 AAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 181

QY 113 GTCTTCCCAGCTCACAAT 131
Db 183 GACTACTGAGTTGGAAGAT 200

RESULT 5
US-60-568-845-22851
; Sequence 22851, Application US/60568845
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/60/568,845
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 39608
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22851
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-568-845-22851

Query Match      20.1%; Score 31; DB 7; Length 201;
Best Local Similarity 62.0%; Pred. No. 0.51;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 53 AATGCATGCAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCACAT 112
Db 122 AAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 181

QY 113 GTCTTCCCAGCTCACAAT 131
Db 182 GACTACTGAGTTGGAAGAT 200

RESULT 6
US-60-568-845-22854
; Sequence 22854, Application US/60568845
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/60/568,845
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 39608
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22854
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-568-845-22854

Query Match      20.1%; Score 31; DB 7; Length 201;
Best Local Similarity 62.0%; Pred. No. 0.51;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 53 AATGCATGCAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCACAT 112
Db 122 AAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 181

QY 113 GTCTTCCCAGCTCACAAT 131
Db 182 GACTACTGAGTTGGAAGAT 200
```



```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22842
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-568-845-22842

```

Query Match 19.7%; Score 30.4; DB 7; Length 201;  
Best Local Similarity 63.9%; Pred. No. 0.83;  
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 53 AATGCATGCAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTAT 112

Db 126 AAGGAAGGAAGGAGGAAGGAAGAAGAAGAAAGACAGGAAAACAGAAACATTTGCAACAAT 185

Qy	113	GTCTTCCAGCT	124
Db	186	GACTACTGAGTT	197

RESULT 12  
US-60-568-845-22845  
; Sequence 22845, Application US/60568845  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

```

/ FILE REFERENCE: CL001524
/ CURRENT APPLICATION NUMBER: US/60/568,845
/ CURRENT FILING DATE: 2004-05-07
/ NUMBER OF SEQ ID NOS: 39608
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 22845
/ LENGTH: 201
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-60-568-845-22845

```

Query Match 19.7%; Score 30.4; DB 7; Length 201;  
Best Local Similarity 63.9%; Pred. No. 0.83;  
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY		53	AATGCTGCAGGAACCAATGCAGAAACCCTTGAAGAGCAGAACAAGCATTTGCCA	TAT	112
Dδ		125	AAGGAAGGAGGAGGAAGGAAGAAAGAACAGAGGAAAACAAGAACTTGCAACA	T	184

Qy 113 GTCTTCCAGCT 124  
| | | | |  
Db 185 GACTACTGAGTT 196

```

RESULT 13
PCT-US03-41761-31797/c
; Sequence 31797, Application PC/JTUS0341761
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: CHARTERIS, Paul
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED
; FILE REFERENCE: MM11150W0
; CURRENT APPLICATION NUMBER: PCT/US03/41761
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31797
; LENGTH: 1207
; TYPE: DNA
; ORGANISM: Bovine 19866880664695

```

PCT-US03-41761-31797

```
Query Match      19.7%; Score 30.4; DB 1; Length 1207;
Best Local Similarity 53.3%; Pred. No. 1.7;
Matches 64; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
```

Qy 9 GCAGAGACCAAGTGGACATGTCAGGAGTTTGTGGAAACAACATGCATGCAGGAACC 68  
Db 372 GCCATGGAAAACTGCCAGATGGTAATGAATTTAGCCACTGCTGACTTCAGCTGGATAC 312

Qy  
69 AATGCAGAAACCTTGAAGAGCAGAACAACGATCTTGCAACTATGTCTTCCAGCTCAC 128

Dd  
312 AAACAAATGACCTTAAGGAGACCAGATTCCATATCTTACTTAATCCCTTCAGCTAAC 253

RESULT 14

PCT-US03-41761-31797/c  
; Sequence 31797, Application PC/TUS0341761

```

: GENERAL INFORMATION:
:
: APPLICANT: MMI GENOMICS, INC.
: APPLICANT: DeNise, Sue K.
: APPLICANT: CHASTERIS, Paul
: APPLICANT: ROSENFIELD, David
: APPLICANT: HOLM, Tom
: APPLICANT: BATES, Stephen
:
: TITLE OF INVENTION: COMPOSITIONS OF MATTER
: FILE REFERENCE: MM11150W
: CURRENT APPLICATION NUMBER: P
: CURRENT FILING DATE: 2003-12
: PRIOR APPLICATION NUMBER: US
: PRIOR FILING DATE: 2002-12-31
: NUMBER OF SEQ ID NOS: 64922
: SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 31797
; LENGTH: 1207
; TYPE: DNA
; ORGANISM: Bovine
PCT-US03-41761-31797
19866880664695

```

```
Query Match      19.7%; Score 30.4; DB 1; Length 1207;
Best Local Similarity 53.3%; Pred.No. 1.7;
Matches 64; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
```

**QY** 9 GGGAGACCAACTGGGACATGTCTCAGGAGTTTGTGGGAACAACANTGCATTCACGAGACC 68  
| | | | | | | | | | | | | | | | | | | | |  
**Dδ** 372 GCCATGGAAAAAAGCTGCCAGATGGTAATGAATTTAGCCACTGTGACTTGACTCGCTGGATTAC 313  
| | | | | | | | | | | | | | | | | | | | |

[illegible]

RESULT 15

```

US-60-568-945-22830
; Sequence 22830, Application US/60568845
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CI001524
; CURRENT APPLICATION NUMBER: US/60/568,845
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 39608
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22830
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-568-945-22830

```

```
Query Match      19.5%; Score 30; DB 7; Length 201;
Best Local Similarity 64.3%; Pred. No. 1.1;
Matches 45; Conservative 0; Mismatches 25; Indels 0; Caps 0;
```



GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:05:11 ; Search time 1282.4 Seconds

(without alignments)  
3586.070 Million cell updates/sec

Title: US-10-681-972-12\_COPY\_116\_269

Perfect score: 154

Sequence: 1 aaggttgcgagagaccaa.....ttgttacttccatgttaa 154

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

E8T:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vri:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122.6	79.6	418	14	CD832625
2	122.6	79.6	419	14	CD834168
3	122.6	79.6	420	14	CD833944
4	122.6	79.6	421	14	CD826491

5	122.6	79.6	421	14	CD831111
6	122.6	79.6	421	14	CD833977
7	122.6	79.6	422	14	CD831972
8	122.6	79.6	422	14	CD833983
9	122.6	79.6	426	14	CD827413
10	122.6	79.6	438	14	CD831479
11	122.6	79.6	446	14	CD834068
12	122.6	79.6	447	14	CD832592
13	122.6	79.6	452	14	CD832071
14	122.6	79.6	453	14	CD834008
15	122.6	79.6	458	14	CD834994
16	122.6	79.6	470	14	CD831680
17	122.6	79.6	553	14	CD831014
18	122.6	79.6	803	28	BH458392
19	121	78.6	408	14	CD833779
20	121	78.6	409	14	CD834090
21	121	78.6	421	14	CD837517
22	121	78.6	424	14	CD833048
23	121	78.6	438	14	CD831294
24	121	78.6	450	14	CD834611
25	121	78.6	480	14	CD828332
26	119.4	77.5	318	9	AA713157
27	119.4	77.5	394	12	BG321454
28	119.4	77.5	421	9	AV816118
29	119.4	77.5	422	9	AV787956
30	119.4	77.5	441	14	CB263345
31	119.4	77.5	519	14	CD835064
32	117.8	76.5	344	29	CC883756
33	117.8	76.5	344	14	Z29957
34	117.8	76.5	400	14	T04323
35	117.8	76.5	403	14	Z27258
36	117.8	76.5	422	9	AV788559
37	117.8	76.5	422	9	AV789144
38	117.8	76.5	435	14	CB259179
39	113.8	73.9	410	12	BG321515
40	113	73.4	346	14	CA992140
41	113	73.4	457	14	CD831226
42	113	73.4	473	14	CD834995
43	113	73.4	476	14	CD833784
44	113	73.4	476	14	CD834092
45	113	73.4	481	14	CD833924

#### ALIGNMENTS

RESULT 1  
CD832625  
LOCUS  
DEFINITION  
BN40.064A14F011227 BN40 Brassica napus CDNA clone BN40064A14, mRNA  
418 bp mRNA linear EST 10-JUL-2003  
sequence.  
CD832625  
CD832625.1 GI:32514565  
EST.  
SOURCE  
Brassica napus (rape)  
ORGANISM  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Genoplatte, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplatte  
Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>) and <http://genoplatte-info.infobiogen.fr>.  
Location/Qualifiers  
1. .418  
source



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/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN4006A14"
/tissue_type="seed"
/clone_lib="BN40"

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## ORIGIN

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Query Match      79.6%; Score 122.6; DB 14; Length 418;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACAATGCATGC 61
Db   143 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 202

QY  62 AGGAACCAATGCAGAACCTTGAAGAGCAGACACGGATCTTGCACATATGTTCTTCCCA 121
Db   203 AAGNATCAGTGCAATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 262

QY  122 GCTCAAAATGATTTTGTACTTCCCATGTTAA 154
Db   263 GCTCAAAATGATTTTGTACTTCCCTGTTAA 295

```

## RESULT 2

```

CD834168
LOCUS      419 bp      mRNA      linear      EST 10-JUL-2003
DEFINITION BN45.040N06F011018 BN45 Brassica napus cDNA clone BN45040N06, mRNA
sequence.
ACCESSION  CD834168
VERSION     CD834168.1
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
ORGANISM    Brassica napus

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

```

```

1 (bases 1 to 419)

```

## REFERENCE

```

AUTHORS      Genoplante, a major partnership french program in plant genomics
TITLE        Unpublished (2003)
JOURNAL      Contact: Genoplante
COMMENT      Genoplante
              93, rue Henri Rochefort 91025 EVRY CEDEX France
              Tel: 33 1 69 47 54 00
              Fax: 33 1 69 47 54 10
              This sequence has been generated in the framework of the french
              plant genomics programme 'Genoplante' (http://www.genoplante.com
              and http://genoplante-info.infobiogen.fr).

```

## FEATURES

```

source
1..419
    location/Qualifiers
    /organism="Brassica napus"
    /mol_type="mRNA"
    /cultivar="Jet neuf"
    /db_xref="taxon:3708"
    /clone="BN45040N06"
    /tissue_type="seed"
    /clone_lib="BN45"

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## ORIGIN

```

Query Match      79.6%; Score 122.6; DB 14; Length 419;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACAATGCATGC 61
Db   140 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 199

QY  62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATATGTTCTTCCCA 121
Db   200 AAGNATCAGTGCAATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 259

```

```

QY  122 GCTCAAAATGATTTTGTACTTCCCATGTTAA 154
Db   260 GCTCAAAATGATTTTGTACTTCCCTGTTAA 292

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## RESULT 3

```

CD833944
LOCUS      420 bp      mRNA      linear      EST 10-JUL-2003
DEFINITION BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
sequence.
ACCESSION  CD833944
VERSION     CD833944.1
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
ORGANISM    Brassica napus

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

```

```

1 (bases 1 to 420)

```

## REFERENCE

```

AUTHORS      Genoplante, a major partnership french program in plant genomics
TITLE        Unpublished (2003)
JOURNAL      Contact: Genoplante
COMMENT      Genoplante
              93, rue Henri Rochefort 91025 EVRY CEDEX France
              Tel: 33 1 69 47 54 00
              Fax: 33 1 69 47 54 10
              This sequence has been generated in the framework of the french
              plant genomics programme 'Genoplante' (http://www.genoplante.com
              and http://genoplante-info.infobiogen.fr).

```

## FEATURES

```

source
1..420
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    /organism="Brassica napus"
    /mol_type="mRNA"
    /cultivar="Jet neuf"
    /db_xref="taxon:3708"
    /clone="BN45040B07"
    /tissue_type="seed"
    /clone_lib="BN45"

```

## ORIGIN

```

Query Match      79.6%; Score 122.6; DB 14; Length 420;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACAATGCATGC 61
Db   140 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 199

QY  62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATATGTTCTTCCCA 121
Db   200 AAGNATCAGTGCAATTAACCTTGAGAAAGCAGACATGGATCTTGCACATATGTTCTTCCCA 259

QY  122 GCTCAAAATGATTTTGTACTTCCCATGTTAA 154
Db   260 GCTCAAAATGATTTTGTACTTCCCTGTTAA 292

```

## RESULT 4

```

CD826491
LOCUS      421 bp      mRNA      linear      EST 10-JUL-2003
DEFINITION BN25.064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA
sequence.
ACCESSION  CD826491
VERSION     CD826491.1
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
ORGANISM    Brassica napus

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

```

```

1 (bases 1 to 421)

```

## REFERENCE

```

AUTHORS      Genoplante, a major partnership french program in plant genomics
TITLE        Unpublished (2003)
JOURNAL      Contact: Genoplante
COMMENT      Genoplante
              93, rue Henri Rochefort 91025 EVRY CEDEX France
              Tel: 33 1 69 47 54 00
              Fax: 33 1 69 47 54 10
              This sequence has been generated in the framework of the french
              plant genomics programme 'Genoplante' (http://www.genoplante.com
              and http://genoplante-info.infobiogen.fr).

```

```

AUTHORS
TITLE      Genoplatte, a major partnership french program in plant genomics
COMMENT    Unpublished (2003)
          Contact: Genoplatte
          Genoplatte
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplatte' (http://www.genoplatte.com
          and http://genoplatte-info.infobiogen.fr).
FEATURES
source
1. .421
   /organism="Brassica napus"
   /mol_type="mRNA"
   /cultivar="Jet neuf"
   /db_xref="taxon:3708"
   /clone="BN25064A05"
   /tissue_type="seed"
   /clone_lib="BN25"

ORIGIN
Query Match      79.6%; Score 122.6; DB 14; Length 421;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGAACAACAATGCATGC 61
    |||
Db  141 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGC 200
    |||

QY  62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGAGATCTTGCACATATGTCTTCCCA 121
    |||
Db  201 AAGAATCAGTGCATTAACCTTGAAGAAAGCAGACATGTAICTTGCACATATGTCTTCCCA 260
    |||

QY  122 GCTCACAAGTGTATTGCTACTTCCCATGTAA 154
    |||
Db  261 GCTCACAAGTGTATTGCTACTTCCCTTTGAAA 293
    |||

RESULT 5
CD831111
LOCUS      CD831111
DEFINITION BN40.058A09F011019 BN40 Brassica napus cDNA clone BN40058A09, mRNA
sequence.
ACCESSION  CD831111
VERSION    CD831111.1 GI:32513051
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS    Genoplatte, a major partnership french program in plant genomics
TITLE      Unpublished (2003)
JOURNAL
COMMENT    Contact: Genoplatte
           Genoplatte
           93, rue Henri Rochefort 91025 EVRY CEDEX France
           Tel: 33 1 69 47 54 00
           Fax: 33 1 69 47 54 10
           This sequence has been generated in the framework of the french
           plant genomics programme 'Genoplatte' (http://www.genoplatte.com
           and http://genoplatte-info.infobiogen.fr).
FEATURES
source
1. .421
   /organism="Brassica napus"
   /mol_type="mRNA"
   /cultivar="Jet neuf"
   /db_xref="taxon:3708"
   /clone="BN40058A09"
   /tissue_type="seed"
   /clone_lib="BN40"

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## ORIGIN

```

Query Match      79.6%; Score 122.6; DB 14; Length 421;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGAACAACAATGCATGC 61
    |||
Db  141 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGC 200
    |||

QY  62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGAGATCTTGCACATATGTCTTCCCA 121
    |||
Db  201 AAGAATCAGTGCATTAACCTTGAAGAAAGCAGACATGTAICTTGCACATATGTCTTCCCA 260
    |||

QY  122 GCTCACAAGTGTATTGCTACTTCCCATGTAA 154
    |||
Db  261 GCTCACAAGTGTATTGCTACTTCCCTTTGAAA 293
    |||

```

## RESULT 6

```

CD833977
LOCUS      CD833977
DEFINITION BN45.040D05F011019 BN45 Brassica napus cDNA clone BN45040D05, mRNA
sequence.
ACCESSION  CD833977
VERSION    CD833977.1 GI:32515917
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS    Genoplatte, a major partnership french program in plant genomics
TITLE      Unpublished (2003)
JOURNAL
COMMENT    Contact: Genoplatte
           Genoplatte
           93, rue Henri Rochefort 91025 EVRY CEDEX France
           Tel: 33 1 69 47 54 00
           Fax: 33 1 69 47 54 10
           This sequence has been generated in the framework of the french
           plant genomics programme 'Genoplatte' (http://www.genoplatte.com
           and http://genoplatte-info.infobiogen.fr).
FEATURES
source
1. .421
   /organism="Brassica napus"
   /mol_type="mRNA"
   /cultivar="Jet neuf"
   /db_xref="taxon:3708"
   /clone="BN45040D05"
   /tissue_type="seed"
   /clone_lib="BN45"

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## ORIGIN

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Query Match      79.6%; Score 122.6; DB 14; Length 421;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGAACAACAATGCATGC 61
    |||
Db  141 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGC 200
    |||

QY  62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGAGATCTTGCACATATGTCTTCCCA 121
    |||
Db  201 AAGAATCAGTGCATTAACCTTGAAGAAAGCAGACATGTAICTTGCACATATGTCTTCCCA 260
    |||

QY  122 GCTCACAAGTGTATTGCTACTTCCCATGTAA 154
    |||
Db  261 GCTCACAAGTGTATTGCTACTTCCCTTTGAAA 293
    |||

```

## RESULT 7

```

CD831972
LOCUS
DEFINITION
  BN40.061108F011228 BN40 Brassica napus cDNA clone BN40061108, mRNA
  sequence.
ACCESSION
  CD831972
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 422)
AUTHORS
  Genoplante.
TITLE
  Genoplante, a major partnership french program in plant genomics
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Genoplante
  Genoplante
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00
  Fax: 33 1 69 47 54 10
  This sequence has been generated in the framework of the french
  plant genomics programme 'Genoplante' (http://www.genoplante.com
  and http://genoplante-info.infobiogen.fr).

FEATURES
  source
    location/Qualifiers
      1..422
        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultivar="Jet neuf"
        /db_xref="taxon:3708"
        /clone="BN40061108"
        /tissue_type="seed"
        /clone_lib="BN40"

ORIGIN
  Query Match 79.6%; Score 122.6; DB 14; Length 422;
  Best Local Similarity 87.6%; Pred. No. 6.2e-27;
  Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

  QY 2 AGTTGTGGGAGAGACCAAGTGGACATGTCAGGAGTTGTGGGAAACAACATGATGC 61
  DB 141 AAGTTGTGGGAGAGCCAAAGTGGACATGTCAGGAGTTGTGGGAAACAACATGATGC 200

  QY 62 AGAACCAATGCGAACAACCTTGAAAGAGCAGAACACGAGTCTTGCAACTATGTTCCCA 121
  DB 201 AAGAATCAGTGCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGTTCCCA 260

  QY 122 GCTCACAATGATTTGTTACTTCCCATCTTAA 154
  DB 261 GCTCACAAGTGTATTGCTACTTCCCTTGTAA 293

RESULT 8
LOCUS
DEFINITION
  BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
  sequence.
ACCESSION
  CD827413
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 426)
AUTHORS
  Genoplante.
TITLE
  Genoplante, a major partnership french program in plant genomics
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Genoplante
  Genoplante
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00
  Fax: 33 1 69 47 54 10
  This sequence has been generated in the framework of the french
  plant genomics programme 'Genoplante' (http://www.genoplante.com
  and http://genoplante-info.infobiogen.fr).

FEATURES
  source
    location/Qualifiers
      1..426
        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultivar="Jet neuf"
        /db_xref="taxon:3708"
        /clone="BN25067G02"
        /tissue_type="seed"
        /clone_lib="BN25"

ORIGIN
  Query Match 79.6%; Score 122.6; DB 14; Length 426;
  Best Local Similarity 87.6%; Pred. No. 6.2e-27;
  Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

  QY 2 AGTTGTGGGAGAGACCAAGTGGACATGTCAGGAGTTGTGGGAAACAACATGATGC 61
  DB 141 AAGTTGTGGGAGAGCCAAAGTGGACATGTCAGGAGTTGTGGGAAACAACATGATGC 200

  QY 62 AGAACCAATGCGAACAACCTTGAAAGAGCAGAACACGAGTCTTGCAACTATGTTCCCA 121
  DB 201 AAGAATCAGTGCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGTTCCCA 260

  QY 122 GCTCACAATGATTTGTTACTTCCCATCTTAA 154
  DB 261 GCTCACAAGTGTATTGCTACTTCCCTTGTAA 293

RESULT 8
LOCUS
DEFINITION
  BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA
  sequence.
ACCESSION
  CD833983
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 422)
AUTHORS
  Genoplante.
TITLE
  Genoplante, a major partnership french program in plant genomics
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Genoplante
  Genoplante
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00

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```

Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
  source
    location/Qualifiers
      1..422
        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultivar="Jet neuf"
        /db_xref="taxon:3708"
        /clone="BN45040D11"
        /tissue_type="seed"
        /clone_lib="BN45"

ORIGIN
  Query Match 79.6%; Score 122.6; DB 14; Length 422;
  Best Local Similarity 87.6%; Pred. No. 6.2e-27;
  Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

  QY 2 AGTTGTGGGAGAGACCAAGTGGACATGTCAGGAGTTGTGGGAAACAACATGATGC 61
  DB 141 AAGTTGTGGGAGAGCCAAAGTGGACATGTCAGGAGTTGTGGGAAACAACATGATGC 200

  QY 62 AGAACCAATGCGAACAACCTTGAAAGAGCAGAACACGAGTCTTGCAACTATGTTCCCA 121
  DB 201 AAGAATCAGTGCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGTTCCCA 260

  QY 122 GCTCACAATGATTTGTTACTTCCCATCTTAA 154
  DB 261 GCTCACAAGTGTATTGCTACTTCCCTTGTAA 293

RESULT 9
LOCUS
DEFINITION
  BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
  sequence.
ACCESSION
  CD827413
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 426)
AUTHORS
  Genoplante.
TITLE
  Genoplante, a major partnership french program in plant genomics
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Genoplante
  Genoplante
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00
  Fax: 33 1 69 47 54 10
  This sequence has been generated in the framework of the french
  plant genomics programme 'Genoplante' (http://www.genoplante.com
  and http://genoplante-info.infobiogen.fr).

FEATURES
  source
    location/Qualifiers
      1..426
        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultivar="Jet neuf"
        /db_xref="taxon:3708"
        /clone="BN25067G02"
        /tissue_type="seed"
        /clone_lib="BN25"

ORIGIN
  Query Match 79.6%; Score 122.6; DB 14; Length 426;
  Best Local Similarity 87.6%; Pred. No. 6.2e-27;
  Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

  QY 2 AGTTGTGGGAGAGACCAAGTGGACATGTCAGGAGTTGTGGGAAACAACATGATGC 61

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Db 141 AAGTTGTGGGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 200
QY 62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGAGATCTTGCAACTATGCTTCCCA 121
Db 201 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTCCCA 260
QY 122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154
Db 261 GCTCAAAAGTGTATTGCTACTTCCCTTGTAA 293

RESULT 10
CD831479
LOCUS
DEFINITION BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA
sequence.
ACCESSION CD831479
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.

FEATURES
source
location/Qualifiers
1..438
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40059J13"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Query Match 79.6%; Score 122.6; DB 14; Length 438;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGGGAGACCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 61
Db 156 AAGTTGTGGGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 215
QY 62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGAGATCTTGCAACTATGCTTCCCA 121
Db 216 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTCCCA 275
QY 122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154
Db 276 GCTCAAAAGTGTATTGCTACTTCCCTTGTAA 308

RESULT 12
CD832592
LOCUS
DEFINITION BN40.063O15F011228 BN40 Brassica napus cDNA clone BN40063O15, mRNA
sequence.
ACCESSION CD832592
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.

FEATURES
source
location/Qualifiers
1..447
/organism="Brassica napus"

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SOURCE
ORGANISM
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://www.genoplante.com.

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location/Qualifiers
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/clone="BN45040H17"
/tissue_type="seed"
/clone_lib="BN45"

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Best Local Similarity 87.6%; Pred. No. 6.3e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGGGAGACCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 61
Db 156 AAGTTGTGGGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 215
QY 62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGAGATCTTGCAACTATGCTTCCCA 121
Db 216 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTCCCA 275
QY 122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154
Db 276 GCTCAAAAGTGTATTGCTACTTCCCTTGTAA 308

RESULT 12
CD832592
LOCUS
DEFINITION BN40.063O15F011228 BN40 Brassica napus cDNA clone BN40063O15, mRNA
sequence.
ACCESSION CD832592
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://www.genoplante.com.

FEATURES
source
location/Qualifiers
1..447
/organism="Brassica napus"

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Best Local Similarity 87.6%; Pred. No. 6.3e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAACAACATGCATGC 61
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QY  62 AGGAACCAATGCAGAAACCTTGAAGAGACGACACGAGTCTTCAACTATGCTTCCCA 121
Db  215 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGATCTTCAACTATGCTTCCCA 274

QY  122 GCTCACAATGTATTGTTACTTCCCATGTTAA 154
Db  275 GCTCACAAGTGTATTGTTACTTCCCTGTGTTAA 307

RESULT 13
CD832071
LOCUS          452 bp      mRNA      linear      EST 10-JUL-2003
DEFINITION    BN40.061003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA
sequence.
ACCESSION    CD832071
VERSION      CD832071.1 GI:32514011
KEYWORDS     EST.
SOURCE       Brassica napus (rape)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
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/organism="Brassica napus"
/mol_type="mRNA"
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/tissue_type="seed"
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Best Local Similarity 87.6%; Pred. No. 6.3e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAACAACATGCATGC 61
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QY  62 AGGAACCAATGCAGAAACCTTGAAGAGACGACACGAGTCTTCAACTATGCTTCCCA 121
Db  220 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGATCTTCAACTATGCTTCCCA 279

RESULT 14
CD834008
LOCUS          453 bp      mRNA      linear      EST 10-JUL-2003
DEFINITION    BN45.040618F011019 BN45 Brassica napus cDNA clone BN45040618, mRNA
sequence.
ACCESSION    CD834008
VERSION      CD834008.1 GI:32515948
KEYWORDS     EST.
SOURCE       Brassica napus (rape)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
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/organism="Brassica napus"
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/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040618"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match          79.6%; Score 122.6; DB 14; Length 453;
Best Local Similarity 87.6%; Pred. No. 6.3e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAACAACATGCATGC 61
Db  141 AAGTTGTGCGAGAGAGCCCAAGTGGGACATGTCAGAGTCTGTGGAACAATAACGCATGC 200

QY  62 AGGAACCAATGCAGAAACCTTGAAGAGACGACACGAGTCTTCAACTATGCTTCCCA 121
Db  201 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGATCTTCAACTATGCTTCCCA 260

QY  122 GCTCACAATGTATTGTTACTTCCCATGTTAA 154
Db  261 GCTCACAAGTGTATTGTTACTTCCCTGTGTTAA 293

RESULT 15
CD834994
LOCUS          458 bp      mRNA      linear      EST 10-JUL-2003
DEFINITION    BN45.043006F011229 BN45 Brassica napus cDNA clone BN45043006, mRNA
sequence.
ACCESSION    CD834994
VERSION      CD834994.1 GI:32516934
KEYWORDS     EST.
SOURCE       Brassica napus (rape)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS

```

TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
1. 458  
Location/Qualifiers  
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/mol\_type="mRNA"  
/cultivar="Jet neuf"  
/db\_xref="taxon:3708"  
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ORIGIN

Query Match 79.6%; Score 122.6; DB 14; Length 458;  
Best Local Similarity 87.6%; Pred. No. 6.3e-27;  
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 2 AGCTTGTCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATGC 61  
Db 156 AAGTTGTGCGAGAGAGCCAAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 215  
Qy 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATATGTCTTCCCA 121  
Db 216 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGGATCTTGCACATATGTCTTCCCA 275  
Qy 122 GCTCACAATGATTTGTGTACTTCCCATGTTAA 154  
Db 276 GCTCACAAGTGATTTGTGTACTTCCCTTGTTAA 308

Search completed: May 18, 2004, 19:00:30  
Job time : 1283.4 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 18, 2004, 19:02:23 ; Search time 2171 Seconds  
(without alignments)  
998.227 Million cell updates/sec

Title: US-10-681-972-2

Perfect score: 305  
Sequence: 1 RLCPSPGTSWGVCGNNAC.....EHGSCNVVFAHKICVFFC 50

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/US10681972/runat\_17052004\_151739\_4351/app\_query\_fasta\_1.199  
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
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10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
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36: em.htg\_man.\*  
37: em.htg\_vrt.\*  
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40: em.htgo\_mus.\*  
41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	305	100.0	270	6	AR014691 Sequence
2	305	100.0	270	6	AR432391 Sequence
3	305	100.0	286	6	AR014689 Sequence
4	305	100.0	286	6	AR432389 Sequence
5	296	97.0	500	6	AR014686 Sequence
6	296	97.0	500	6	AR432386 Sequence
7	283	92.8	285	6	AR014692 Sequence
8	283	92.8	285	6	AR432392 Sequence
9	283	92.8	395	8	RSU18557
10	283	92.8	414	6	A26875
11	283	92.8	414	6	A39549
12	283	92.8	414	6	A63404
13	283	92.8	414	6	AR050153
14	283	92.8	414	6	AR130272
15	283	92.8	414	6	I23728 Sequence 48
16	283	92.8	414	6	AR207337 Sequence
17	283	92.8	414	6	AR374914 Sequence
18	278	91.1	243	6	AX412406 Sequence
19	278	91.1	243	6	AX412601 Sequence
20	278	91.1	243	6	AX651878 Sequence
21	278	91.1	243	8	AY060506 Arabidops
22	278	91.1	403	6	A68645 Sequence 13
23	278	91.1	403	8	ATANTSPEC
24	278	91.1	425	8	AY052236 Arabidops
25	278	91.1	471	11	BV010672 MASC STS1
26	278	91.1	563	11	BV010667 MASC STS1
27	278	91.1	572	11	BV010673 MASC STS1
28	278	91.1	578	11	BV010671 MASC STS1
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31	278	91.1	95870	8	AC007396 Genomic s
32	277	90.8	933	8	BOL311046 Brassica
33	274	89.8	285	6	AR014693 Sequence
34	274	89.8	285	6	AR432393 Sequence
35	274	89.8	288	6	A39553 Sequence 41
36	274	89.8	288	6	AR050161 Sequence
37	274	89.8	288	6	AR130280 Sequence
38	274	89.8	288	6	I23736 Sequence 58
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40	274	89.8	457	8	RSU18556
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ALIGNMENTS

RESULT 1

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DEFINITION Sequence 14 from patent US 5773696.
ACCESSION AR014691
VERSION AR014691.1 GI:3972145
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 270)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., and Rosenberger, C.A.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 14 30-JUN-1998;
FEATURES
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Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 109 AGTTGTGCGAGACCAAGTGGACATGTCAGGAGTTTGTGGAAACAACATGCATGC 168
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 169 AGAACCAATGCAGAACCACTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 228
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 229 GCTCACAAATGATTGTTACTTCCCATGT 258
RESULT 2
LOCUS AR432391 270 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6653280.
ACCESSION AR432391
VERSION AR432391.1 GI:40194668
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 270)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., and Rosenberger, C.A.
TITLE Antifungal polypeptide AlyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 14 25-NOV-2003;
FEATURES
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Pred. No.: 3.38e-27 Length: 270
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-681-972-2 (1-50) x AR432391 (1-270)

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QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 169 AGAACCAATGCAGAACCACTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 228
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 229 GCTCACAAATGATTGTTACTTCCCATGT 258
RESULT 3
LOCUS AR014689 286 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 12 from patent US 5773696.
ACCESSION AR014689
VERSION AR014689.1 GI:3972143
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 286)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., and Rosenberger, C.A.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 12 30-JUN-1998;
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 177 AGAACCAATGCAGAACCACTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 236
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 237 GCTCACAAATGATTGTTACTTCCCATGT 266
RESULT 4
LOCUS AR432389 286 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6653280.
ACCESSION AR432389
VERSION AR432389.1 GI:40194666
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 286)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., and Rosenberger, C.A.
TITLE Antifungal polypeptide AlyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 12 25-NOV-2003;
FEATURES
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## Alignment Scores:

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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

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 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
 Db 177 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCAACTATGTCTTCCCA 236  
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
 Db 237 GCTCACAAATGTATTGTACTTCCCATGT 266

## RESULT 5

## AR014686

## LOCUS

DEFINITION Sequence 9 from patent US 5773696. linear PAT 05-DEC-1998

## ACCESSION

## AR014686

## VERSION

## AR014686.1

## KEYWORDS

## SOURCE

## ORGANISM

## Unknown.

## REFERENCE

## 1 (bases 1 to 500)

## AUTHORS

## Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.

## TITLE

## Antifungal polypeptide and methods for controlling plant pathogenic fungi

## JOURNAL

## Patent: US 5773696-A 9 30-JUN-1998;

## FEATURES

## Location/Qualifiers

## 1..500

## /organism="unknown"

## /mol\_type="unassigned DNA"

## ORIGIN

## Alignment Scores:

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 Percent Similarity: 98.00% Conservative: 1  
 Best Local Similarity: 96.00% Mismatches: 1  
 Query Match: 97.05% Indels: 0  
 DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR014686 (1-500)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
 Db 159 AAGTTGTGCGAGAGTCCAAAGTGGAAACATGCTCAGGCGTGTGGGAATAATAACGCATGC 218  
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
 Db 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCAACTATGTCTTCCCA 278  
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
 Db 279 GCTCACAAATGTATTGTACTTCCCATGT 308

## RESULT 6

## AR432386

## LOCUS

DEFINITION Sequence 9 from patent US 6653280. linear PAT 18-DEC-2003

## ACCESSION

## AR432386

VERSION AR432386.1 GI:40194663

## KEYWORDS

## SOURCE

## ORGANISM

## Unknown.

## REFERENCE

## 1 (bases 1 to 500)

## AUTHORS

## Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.

## TITLE

## Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi

## JOURNAL

## Patent: US 6653280-A 9 25-NOV-2003;

## FEATURES

## Location/Qualifiers

## 1..500

## /organism="unknown"

## /mol\_type="genomic DNA"

## ORIGIN

## Alignment Scores:

Pred. No.: 7 95e-26 Length: 500  
 Score: 296.00 Matches: 48  
 Percent Similarity: 98.00% Conservative: 1  
 Best Local Similarity: 96.00% Mismatches: 1  
 Query Match: 97.05% Indels: 0  
 DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR432386 (1-500)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
 Db 159 AAGTTGTGCGAGAGTCCAAAGTGGAAACATGCTCAGGCGTGTGGGAATAATAACGCATGC 218  
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
 Db 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCAACTATGTCTTCCCA 278  
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
 Db 279 GCTCACAAATGTATTGTACTTCCCATGT 308

## RESULT 7

## AR014692

## LOCUS

## DEFINITION

## Sequence 16 from patent US 5773696. linear PAT 05-DEC-1998

## ACCESSION

## AR014692

## VERSION

## AR014692.1

## KEYWORDS

## SOURCE

## Unknown.

## ORGANISM

## Unknown.

## REFERENCE

## 1 (bases 1 to 285)

## AUTHORS

## Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.

## TITLE

## Antifungal polypeptide and methods for controlling plant pathogenic fungi

## JOURNAL

## Patent: US 5773696-A 16 30-JUN-1998;

## FEATURES

## Location/Qualifiers

## 1..285

## /organism="unknown"

## /mol\_type="unassigned DNA"

## ORIGIN

## Alignment Scores:

Pred. No.: 1 42e-24 Length: 285  
 Score: 283.00 Matches: 45  
 Percent Similarity: 96.00% Conservative: 3  
 Best Local Similarity: 90.00% Mismatches: 2  
 Query Match: 92.79% Indels: 0  
 DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR014692 (1-285)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
 Db 121 AAGTTGTGCGAGAGGCGCATCAGGAGTGTGGTTCAGGAGTCTGCGGAACAACACGCATGC 180

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
 Db 181 AAGAACCAATGATCAACCTCGAGAGGCGGATGATCTGCACTAGCTTCCCA 240  
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
 Db 241 GCTCACAAGTGCATCTGCTACTTTCATGC 270

RESULT 8  
 AR432392  
 LOCUS  
 DEFINITION Sequence 16 from patent US 6653280.  
 ACCESSION AR432392  
 VERSION AR432392.1 GI:40194669  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.  
 REFERENCE 1. (bases 1 to 285)  
 AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.  
 TITLE Antifungal polypeptide AlyAPP from *Alyseum* and methods for  
 controlling plant pathogenic fungi  
 JOURNAL Patent: US 6653280-A 16 25-NOV-2003;  
 FEATURES Location/Qualifiers  
 source  
 1..285  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,42e-24 Length: 285  
 Score: 283.00 Matches: 45  
 Percent Similarity: 96.00% Conservative: 3  
 Best Local Similarity: 90.00% Mismatches: 2  
 Query Match: 92.79% Indels: 0  
 DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR432392 (1-285)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
 Db 121 AAGTTGGCGAGGCGCATCAGGACTTGTCTAGAGTCTGCGGAACACACACGATGC 180  
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
 Db 181 AAGAACCAATGATCAACCTCGAGAGGCGGATGATCTGCACTAGCTTCCCA 240  
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
 Db 241 GCTCACAAGTGCATCTGCTACTTTCATGC 270

RESULT 9  
 RSU18557  
 LOCUS  
 DEFINITION Raphanus sativus antifungal protein 1 preprotein (Rs-APP1) mRNA,  
 complete cds.  
 ACCESSION U18557  
 VERSION U18557.1 GI:644773  
 KEYWORDS  
 SOURCE Raphanus sativus (radish)  
 ORGANISM Raphanus sativus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.  
 REFERENCE 1. (sites)  
 AUTHORS Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,  
 Osborn,R.W., Kester,A., Rees,S.B., Torrekens,S., Van Leuven,F.,  
 Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.  
 TITLE Small cysteine-rich antifungal proteins from radish: their role in  
 host defense  
 JOURNAL Plant Cell 7, 568-573 (1995)  
 REFERENCE 2. (bases 1 to 395)  
 AUTHORS Terras,F.R.

TITLE Direct Submission  
 JOURNAL Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory  
 of Genetics, Applied Biological Sciences, W. De Croylaan 42,  
 Heverlee, Belgium, B-3001  
 COMMENT On Feb 9, 1995 this sequence version replaced gi:609321.  
 FEATURES Location/Qualifiers  
 source  
 1..395  
 /organism="Raphanus sativus"  
 /mol\_type="mRNA"  
 /strain="ronde rode kleine witpunt"  
 /db\_xref="taxon:3726"  
 /tissue\_type="seed"  
 1..395  
 /gene="Rs-APP1"  
 15..257  
 /gene="Rs-APP1"  
 /function="antifungal, fungistatic"  
 /codon\_start=1  
 /evidence=experimental  
 /product="antifungal protein 1 preprotein"  
 /protein\_id="AA69541.1"  
 /db\_xref="GI:609322"  
 /translation="MAKFAIIALLFAALVLFAPFAEAPTMTVEAQLCERPSGTWSGVC  
 GNNACKNQCNINLEAKRHGSCNYVFAHKICIVFPC"  
 15..101  
 /gene="Rs-APP1"  
 102..254  
 /gene="Rs-APP1"  
 /product="antifungal protein 1"  
 /function="antifungal, fungistatic"  
 /note="Evidence for antifungal activity: Analysis of two  
 novel classes of antifungal proteins from radish (*Raphanus  
 sativus* L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.  
 Chem. 267, 15301-15309"  
 /citation=[1]  
 /evidence=experimental  
 395  
 /gene="Rs-APP1"  
 /note="18 A nucleotides"

polyA\_signal  
 395  
 /gene="Rs-APP1"  
 /note="18 A nucleotides"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,07e-24 Length: 395  
 Score: 283.00 Matches: 45  
 Percent Similarity: 96.00% Conservative: 3  
 Best Local Similarity: 90.00% Mismatches: 2  
 Query Match: 92.79% Indels: 0  
 DB: 8 Gaps: 0

US-10-681-972-2 (1-50) x RSU18557 (1-395)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
 Db 105 AAGTTGGCGAAGGCCAAGTGGGATGTCAGGAGTCTGTGGAACAAATAACGATGC 164  
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
 Db 165 AAGAATCAGTCATTAACTTGAAGAAGCACACATGATCTTGTCTTCCCA 224  
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
 Db 225 GCTCACAAGTGCATCTGCTACTTTCCTGT 254

RESULT 10  
 A26875  
 LOCUS  
 DEFINITION R.sativus APP1 gene.  
 ACCESSION A26875  
 VERSION A26875.1 GI:1247352  
 KEYWORDS  
 SOURCE Raphanus sativus (radish)  
 ORGANISM Raphanus sativus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

REFERENCE 1 (bases 1 to 414)

AUTHORS Broekaert, W.F., Cammue, B.P.A., Terras, F.R.G., Vanderleyden, J., Osborn, R.W. and Rees, S.B.

TITLE BIOCIDAL PROTEINS

JOURNAL Patent: WO 9305153-A 33 18-MAR-1993;

FEATURES ICI PLC (GB)

Location/Qualifiers

1. .414

/organism="Raphanus sativus"

/mol\_type="unassigned DNA"

/db\_xref="taxon:3726"

ORIGIN

Alignment Scores:

Pred. No.: 2.18e-24 Length: 414

Score: 283.00 Matches: 45

Percent Similarity: 96.00% Conservative: 3

Best Local Similarity: 90.00% Mismatches: 2

Query Match: 92.79% Indels: 0

DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x A26875 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC 165

Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAATCAGTGCATTAACTTGAAGAAGCAGCATGGATCTTGCAACTATGCTTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 11

LOCUS A39549

DEFINITION Sequence 37 from Patent WO9416076.

ACCESSION A39549

VERSION A39549.1 GI:2295842

KEYWORDS unidentified

SOURCE unclassified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 414)

AUTHORS Dubock, A.C., Powell, K.A. and Rees, S.B.

TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS

JOURNAL Patent: WO 9416076-A 37 21-JUL-1994;

ZENECA LTD (GB)

COMMENT Other publication AU 5820494 940815.

FEATURES Location/Qualifiers

source

1. .414

/organism="unidentified"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32644"

ORIGIN

Alignment Scores:

Pred. No.: 2.18e-24 Length: 414

Score: 283.00 Matches: 45

Percent Similarity: 96.00% Conservative: 3

Best Local Similarity: 90.00% Mismatches: 2

Query Match: 92.79% Indels: 0

DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x A39549 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC 165

Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAATCAGTGCATTAACTTGAAGAAGCAGCATGGATCTTGCAACTATGCTTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 12

LOCUS A63404

DEFINITION Sequence 19 from Patent WO9721814.

ACCESSION A63404

VERSION A63404.1 GI:3717176

KEYWORDS unidentified

SOURCE unclassified

ORGANISM unclassified

REFERENCE 1

AUTHORS Broekaert, W.F., De, S.G., Rees and Sarah, B.

TITLE ANTIFUNGAL PROTEINS

JOURNAL Patent: WO 9721814-A 19 19-JUN-1997;

ZENECA LTD (GB)

COMMENT Other publication AU 1105397 19970703.

FEATURES Location/Qualifiers

source

1. .414

/organism="unidentified"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32644"

ORIGIN

Alignment Scores:

Pred. No.: 2.18e-24 Length: 414

Score: 283.00 Matches: 45

Percent Similarity: 96.00% Conservative: 3

Best Local Similarity: 90.00% Mismatches: 2

Query Match: 92.79% Indels: 0

DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x A63404 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC 165

Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAATCAGTGCATTAACTTGAAGAAGCAGCATGGATCTTGCAACTATGCTTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 13

LOCUS AR050153

DEFINITION Sequence 48 from patent US 5824869.

ACCESSION AR050153

VERSION AR050153.1 GI:5972145

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 414)

AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.

TITLE Biocidal proteins

JOURNAL Patent: US 5824869-A 48 20-OCT-1998;

FEATURES Location/Qualifiers

source

1. .414

/organism="unknown"

/mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores: 2.18e-24 Length: 414  
Pred. No.: 283.00 Matches: 45  
Score: 283.00  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR050153 (1-414)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 106 AAGTTGTGCGAAGGCGCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 165

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 166 AAGATCAGTGCATTAACTTACCTTGAGAAAGCAGACATGGAATCTTGCAACTATGTCTTCCCA 225

QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 226 GCTCACAAGTGTATCTGCTACTTTCTTGT 255

## RESULT 14

LOCUS AR130272 414 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 48 from patent US 6187904.  
ACCESSION AR130272  
VERSION AR130272.1 GI:14118169  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,  
Terras, F.R.G. and Vanderleyden, J.  
TITLE Biocidal proteins  
JOURNAL Patent: US 6187904-A 48 13-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..414  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores: 2.18e-24 Length: 414  
Pred. No.: 283.00 Matches: 45  
Score: 283.00  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR130272 (1-414)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 106 AAGTTGTGCGAAGGCGCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 165

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 166 AAGATCAGTGCATTAACTTACCTTGAGAAAGCAGACATGGAATCTTGCAACTATGTCTTCCCA 225

QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 226 GCTCACAAGTGTATCTGCTACTTTCTTGT 255

## RESULT 15

LOCUS I23728 414 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 48 from patent US 5538525.  
ACCESSION I23728  
VERSION I23728.1 GI:1603598

KEYWORDS  
SOURCE Unknown.ORGANISM  
Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,  
Terras, F.R.G. and Vanderleyden, J.  
TITLE Biocidal proteins  
JOURNAL Patent: US 5538525-A 48 23-JUL-1996;  
FEATURES Location/Qualifiers  
source 1..414  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores: 2.18e-24 Length: 414  
Pred. No.: 283.00 Matches: 45  
Score: 283.00  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x I23728 (1-414)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 106 AAGTTGTGCGAAGGCGCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 165

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 166 AAGATCAGTGCATTAACTTACCTTGAGAAAGCAGACATGGAATCTTGCAACTATGTCTTCCCA 225

QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 226 GCTCACAAGTGTATCTGCTACTTTCTTGT 255

Search completed: May 18, 2004, 21:15:13

Job time : 2173 secs



us-10-681-972-2.p2n.rng

Wed May 19 11:30:05 2004

PA (MONS ) MONSANTO CO.  
 XX  
 PI Liang J, Shah D, Wu Y, Rosenberger CA;  
 XX  
 DR WPI; 1997-503109/46.  
 DR P-PSDB; AAW35560.  
 XX  
 PT Alyssum antifungal polypeptide and corresponding DNA - used in the  
 PT production of transgenic plants resistant to phytopathogenic fungi.  
 XX  
 PS Example 4; Page 69; 92pp; English.  
 XX  
 CC This sequence represents the cDNA sequence cloned into the E. coli  
 CC cassette vector pMON22317 to generate vector pMON22652. The cDNA encodes  
 CC the antifungal polypeptide AlyAFP, isolated from plants of the genus  
 CC Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic  
 CC fungi, whilst the coding DNA can be used to produce transgenic plants  
 CC that express the polypeptide making them resistant to the phytopathogenic  
 CC fungi.  
 XX  
 SQ Sequence 270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;  
 Alignment Scores:  
 Pred. No.: 1.05e-26 Length: 270  
 Score: 305.00 Matches: 50  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-681-972-2 (1-50) x AAT94582 (1-270)  
 QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
 Db 109 AGTTGTGCGAGAGACCAAGTGGCATGCTCAGGAGTTTGGGGAACAACATGCATGC 168  
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
 Db 169 AGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCACATATGCTTCCCA 228  
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
 Db 229 GCTCACAATGATTTGTTACTTCCATGT 258

RESULT 2  
 AAT94574  
 ID AAT94574 standard; cDNA; 286 BP.  
 XX  
 AC AAT94574;  
 XX  
 DT 12-MAY-1998 (first entry)  
 XX  
 DE Alyssum species anti-fungal polypeptide AlyAFP cDNA sequence.  
 XX  
 KW Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;  
 KW phytopathogenic fungus; resistance; ss.  
 XX  
 OS Alyssum sp.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 117..269  
 FT /\*tag= a  
 FT /product= "mature AlyAFP protein"  
 FT /note= "no start codon given at 5' end of sequence"  
 XX  
 XX WO9737024-A2.  
 XX  
 PD 09-OCT-1997.  
 XX  
 XX 27-MAR-1997; 97WO-US005709.  
 XX  
 XX 29-MAR-1996; 96US-00627706.  
 XX

(MONS ) MONSANTO CO.  
 XX  
 PI Liang J, Shah D, Wu Y, Rosenberger CA;  
 XX  
 DR WPI; 1997-503109/46.  
 DR P-PSDB; AAW35558.  
 XX  
 PT Alyssum antifungal polypeptide and corresponding DNA - used in the  
 PT production of transgenic plants resistant to phytopathogenic fungi.  
 XX  
 PS Claim 12; Page 68; 92pp; English.  
 XX  
 CC This sequence encodes the mature protein of an antifungal polypeptide  
 CC (AlyAFP) isolated from plants of the genus Alyssum. The sequence was PCR  
 CC amplified using primers AAT94583-T94584, and the resultant 264 bp  
 CC fragment was cloned as a BamHI fragment into the expression vector  
 CC pMON22317 to generate plasmid pMON22652. The AlyAFP sequence in this  
 CC plasmid is placed under control of an E35S promoter and the maize HSP70  
 CC intron 1 sequence. The protein can be used to control phytopathogenic  
 CC fungi, whilst the DNA can be used to produce transgenic plants that  
 CC express the protein making them resistant to the phytopathogenic fungi.  
 XX  
 SQ Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.13e-26 Length: 286  
 Score: 305.00 Matches: 50  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-681-972-2 (1-50) x AAT94574 (1-286)  
 QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
 Db 117 AGTTGTGCGAGAGACCAAGTGGCATGCTCAGGAGTTTGGGGAACAACATGCATGC 176  
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
 Db 177 AGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCACATATGCTTCCCA 236  
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
 Db 237 GCTCACAATGATTTGTTACTTCCATGT 266

RESULT 3  
 AAT99289  
 ID AAT99289 standard; DNA; 481 BP.  
 XX  
 AC AAT99289;  
 XX  
 DT 12-MAY-1998 (first entry)  
 XX  
 DE Alyssum species AlyAFP cDNA sequence.  
 XX  
 KW Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;  
 KW phytopathogenic fungus; resistance; ss.  
 XX  
 OS Alyssum sp.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 53..292  
 FT /\*tag= a  
 FT /product= "AlyAFP antifungal polypeptide"  
 FT sig\_peptide 53..139  
 FT mat\_peptide 140..289  
 FT polyA\_signal 439..443  
 XX  
 XX WO9737024-A2.  
 XX

```

XX PD 09-OCT-1997.
XX PF 27-MAR-1997; 97WO-US005709.
XX PR 29-MAR-1996; 96US-00627706.
XX PA (MONS ) MONSANTO CO.
XX PI Liang J, Shah D, Wu Y, Rosenberger CA;
XX DR WPI; 1997-503109/46.
XX DR P-PSDB; AAW35560.
XX PT Alyssum antifungal polypeptide and corresponding DNA - used in the
XX PR production of transgenic plants resistant to phytopathogenic fungi.
XX PA Example 4; Fig 1; 92pp; English.
XX CC This sequence represents the cDNA sequence which encodes the antifungal
XX CC polypeptide AlyAPP, isolated from plants of the genus Alyssum. The AlyAPP
XX CC polypeptide can be used to control phytopathogenic fungi, whilst the
XX CC coding DNA can be used to produce transgenic plants that express the
XX CC polypeptide making them resistant to the phytopathogenic fungi
XX SQ Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.14e-26 Length: 481
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-681-972-2 (1-50) x AAT99289 (1-481)
Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 140 AGTTGTGCGAGAGACCAAGTGGACATGTCAGAGTTTGTGGGAACAACAATGCATGC 199
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 200 AGGAACCAATCGAAGAACCTTTGAAGAGCAGACACGAGATCTGCACACTATGTCTTCCCA 259
Qy 41 AlahisLysCysIleCysTyrPheProCys 50
Db 260 GCTCACAATGATTTGTTACTTCCCATGT 289

RESULT 4
AAT94581
ID AAT94581 standard; DNA; 500 BP.
AC AAT94581;
XX 12-MAY-1998 (first entry)
DT 12-MAY-1998 (first entry)
XX Composite cDNA sequence for Alyssum species antifungal polypeptide.
XX Antifungal polypeptide; AlyAPP; inhibition; transgenic plant;
XX phytopathogenic fungus; resistance; ss.
XX Alyssum sp.
XX WO9737024-A2.
XX 09-OCT-1997.
XX 27-MAR-1997; 97WO-US005709.
XX 29-MAR-1996; 96US-00627706.
XX (MONS ) MONSANTO CO.

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XX Liang J, Shah D, Wu Y, Rosenberger CA;
XX WPI; 1997-503109/46.
XX Alyssum antifungal polypeptide and corresponding DNA - used in the
XX production of transgenic plants resistant to phytopathogenic fungi.
XX Example 4; Page 67; 92pp; English.
XX This sequence represents the cDNA sequence encoding the antifungal
XX polypeptide AlyAPP, from plants of the genus Alyssum. The sequence
XX represents a composite of the sequences isolated by 5' and 3' RACE (Rapid
XX Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The
XX AlyAPP polypeptide can be used to control phytopathogenic fungi, whilst
XX the coding DNA can be used to produce transgenic plants that express the
XX polypeptide making them resistant to the phytopathogenic fungi
XX SQ Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.5e-25 Length: 500
Score: 296.00 Matches: 48
Percent Similarity: 98.00% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 1
Query Match: 97.05% Indels: 0
DB: 2 Gaps: 0

US-10-681-972-2 (1-50) x AAT94581 (1-500)
Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCGAGAGTCCCAAGTGGACATGTCAGCGTGTGGGAATAATAACGCATGC 218
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 219 AGGAACCAATCGAAGAACCTTTGAAGAGCAGACACGAGATCTGCACACTATGTCTTCCCA 278
Qy 41 AlahisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAATGATTTGTTACTTCCCATGT 308

RESULT 5
ADC51221
ID ADC51221 standard; DNA; 394 BP.
AC ADC51221;
XX 18-DEC-2003 (first entry)
DT 18-DEC-2003 (first entry)
XX Brassica oleracea defensin protein coding sequence.
XX antimicrobial protein; defensin; transgenic plant;
XX composite disease resistance; pathogenic bacteria;
XX rice white leaf blight; brown-stripe disease; glume blight;
XX seedling damping-off disease; filamentous fungi; rice blight;
XX sheath blight disease; leaf blight; gene; ds.
XX Brassica oleracea.
XX PH Key Location/Qualifiers
XX CDS 1..243
XX FT /*tag= a
XX FT /product= "Brassica oleracea defensin protein"
XX JP2003088379-A.
XX 25-MAR-2003.
XX 18-SEP-2001; 2001JP-00283117.
XX 18-SEP-2001; 2001JP-00283117.
XX

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Wed May 19 11:30:05 2004

(DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

PA WPI: 2003-621123/59.  
DR P-PSDB; ADC51222.

XX Novel protein from *Brassica campestris*, useful as antimicrobial against  
PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for  
PT treating e.g. rice white leaf blight and sheath blight disease.

XX Claim 3; SEQ ID NO 1; 34pp; Japanese.

XX The invention comprises the amino acid and coding sequences of  
CC antimicrobial (defensin) proteins from *Brassica*. The DNA and protein  
CC sequences of the invention are useful for producing transgenic plants  
CC with composite disease resistance, especially resistant to diseases  
CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-  
CC stripe disease, glume blight, and seedling damping-off disease. As well  
CC as diseases caused by filamentous fungi, such as: rice blight, sheath  
CC blight disease, and leaf blight. The present DNA sequence encodes a  
CC *Brassica* defensin protein of the invention.

XX Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Alignment Scores: 394  
Pred. No.: 6.08e-24 Length: 394  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x ADC51221 (1-394)

OY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
DB 91 AAGTTGTCGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC 150  
OY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
DB 151 AAGAATCAGTCATTAACCTTGAGAAAGCAGACATGGATCTTGCACATATGCTCTCCCA 210  
OY 41 AlaHisLysCysIleCysTyrPheProCys 50  
DB 211 GCTCAAGTGTATTTGCTACTTCTCTTCT 240

RESULT 6  
AAQ38650  
ID AAQ38650 standard; DNA; 414 BP.

XX AAQ38650;  
XX AC  
XX 25-MAR-2003 (revised)  
DT 07-JUL-1993 (first entry)  
XX Rs-APPI cDNA.  
XX Raphanus sativus; *Brassica*; Arabidopsis; *Chnicus*; *Lathyrus*; *Clitoria*;  
KW fungicide; bactericide; antibiotic; antifungal; gram positive;  
KW plant disease resistance; low toxicity.

OS Raphanus sativus.  
XX Key Location/Qualifiers  
FH 16..256  
CDS /\*tag= a

XX WO9305153-A1.  
XX 18-MAR-1993.  
XX 27-AUG-1992; 92WO-GB001570.  
XX 29-AUG-1991; 91GB-00018523.

PR 13-FEB-1992; 92GB-00003038.  
PR 25-JUN-1992; 92GB-00013526.

XX (ICIL) IMPERIAL CHEM IND PLC.

XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras PRG;  
PI Vanderleyden J;

XX WPI; 1993-100978/12.

XX Biocidal proteins isolated from seeds of plants - e.g. *brassica* or  
PT dahlia, useful for increasing plants' resistance to fungal and bacterial  
PT diseases.

PS Example 21; Fig 35; 110pp; English.

XX This cDNA represents the sequence of Rs-APPI from *Raphanus sativus*. PCR  
CC primer AAQ38640 was used together with AAQ38641 to generate a probe for  
CC screening a *Raphanus sativus* seed cDNA library. This primer corresponds  
CC to amino acids 2 to 7 of Rs-APPI and has a sense orientation. The 144bp  
CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a  
CC 123bp product, which was further reamplified with the same primers and  
CC digoxigenin-11-dump instead of dTTP to give a digoxigenin labeled PCR  
CC product. This was used to screen a lambda ZAPII cDNA library by in situ  
CC plaque hybridisation. Positive plaques were purified and subjected to two  
CC additional screening rounds with the same probe. Inserts were excised in  
CC vivo into the pBluescript phagemid form with the aid of helper phage  
CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and  
CC their size compared by agarose gel electrophoresis. Four clones had  
CC insert sizes of approx. 400bp the others between 250-300bp. The inserts  
CC of the 4 largest clones were then sequenced and found to differ only in  
CC the length of their 5' and 3' UTR's. The longest sequence is given here.  
CC (Updated on 25-MAR-2003 to correct FN field.)

XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores: 414  
Pred. No.: 6.46e-24 Length: 414  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 2 Gaps: 0

US-10-681-972-2 (1-50) x AAQ38650 (1-414)

OY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
DB 106 AAGTTGTCGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC 165  
OY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
DB 166 AAGAATCAGTCATTAACCTTGAGAAAGCAGACATGGATCTTGCACATATGCTCTCCCA 225  
OY 41 AlaHisLysCysIleCysTyrPheProCys 50  
DB 226 GCTCAAGTGTATTTGCTACTTCTCTTCT 255

RESULT 7  
AAQ70128  
ID AAQ70128 standard; cDNA; 414 BP.

XX AAQ70128;

XX 25-MAR-2003 (revised)  
DT 14-FEB-1995 (first entry)

XX Antimicrobial Rs-APPI.

XX Antimicrobial; Rs-APPI; symbiosis; disease-resistance; fungus-resistance;  
KW *Clavibacter xyli* subsp. *cynodontis*; Cxc; crop improvement; endophyte; ss.  
XX *Raphanus sativus*.  
OS



XX WO9416076-A1.  
PN XX  
PD PD 21-JUL-1994.  
PF XX  
PR XX 05-JAN-1994; 94WO-GB0000012.  
XX XX  
XX XX 08-JAN-1993; 93GB-00000281.  
XX XX  
XX XX (ZENE ) ZENECA LTD.  
XX XX  
XX XX Dubock AC, Powell KA, Rees SB;  
XX XX  
XX XX WPI; 1994-249223/30.  
DR DR P-PSDB; AAR57325.  
XX XX  
XX XX Antimicrobial protein producing endo-symbiotic microorganisms - is  
PT produced by combining nucleic acids encoding the protein with an  
PT endophyte, useful for protecting plant hosts from esp. fungal disease.  
XX XX  
XX XX Disclosure; Page 31; 39pp; English.  
XX XX  
XX XX Plant-derived antimicrobial proteins are expressed in endosymbiotic  
CC Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with  
CC recombinant Cxc are protected against fungal disease. A suitable  
CC antimicrobial protein is Rs-APPl from R. sativus. The full-length cDNA  
CC sequence of Rs-APPl is given in AAQ70128. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX XX  
XX XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 6.46e-24 Length: 414  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: Gaps: 0  
US-10-681-972-2 (1-50) x AAQ70128 (1-414)  
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 165  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 166 AAGAATCAGTGCATTAACTTGAAGAACGACGACATGGATCTTGCAACTATGCTTCCCA 225  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 226 GCTCACAAAGTGTATCTGACTTCTTCTTGT 255  
RESULT 8  
AA72333  
ID AA72333 standard; cDNA; 414 BP.  
XX AC  
XX AAT72333;  
XX XX  
XX XX 25-MAR-2003 (revised)  
DT 19-JAN-1998 (first entry)  
XX XX  
XX XX Raphanus sativus antifungal protein I (Rs-APPl) cDNA.  
DE XX  
XX XX Antifungal protein; candida; fungal resistance; food additive; radish;  
KW crop protection; plant defensin; bacterial protection; preservative; ss.  
XX XX  
XX XX Raphanus sativus.  
XX XX  
XX XX Location/Qualifiers  
FH 16..258  
FT CDS  
FT /\*tag= a  
FT /transl\_except= (pos:85..87, aa:Glu)  
FT

FT sig\_peptide 16..102  
FT /\*tag= b  
FT mat\_peptide 103..255  
FT /\*tag= c  
FT /product= "antifungal\_protein\_1"  
XX  
PN WO9721815-A2.  
XX  
XX 19-JUN-1997.  
PD  
XX 12-DEC-1996; 96WO-GB003068.  
PF  
XX 13-DEC-1995; 95GB-00025455.  
PR 28-MAR-1996; 96GB-00006552.  
XX XX  
XX (ZENE ) ZENECA LTD.  
XX  
XX Melloen RH, Puijk WC, Schaaper WMM, Sijtsma L, Van Amerongen A;  
PI Broekaert W, Samblanx GW, Fant F, Borrenans FAM, Rees SB;  
PI Van Gelder WMJ;  
XX  
XX WPI; 1997-332786/30.  
DR P-PSDB; AAM19280.  
XX  
XX Antifungal peptide derived from radish antifungal protein 2 - and related  
PT DNA, useful for producing plants with increased fungal resistance and as  
PT therapeutic or preservative agent.  
XX  
XX Claim 8; Fig 2; 65pp; English.  
XX  
XX This cDNA sequence encodes an Rhamnus sativus (radish) antifungal  
CC protein (Rs-APPl). Analogues of the homologous protein, RS-APP2  
CC (AAM19281), have also been produced (see AAM19282-92, AAM19294-98,  
CC AAM19301-04, AAM19330-34 and AAM1965-834). Plants containing DNA  
CC sequences encoding these proteins have improved resistance to fungi.  
CC Compositions containing the peptides can be used to control fungi or  
CC bacteria in pharmaceutical (e.g. treatment of Candida infections) or  
CC preservative purposes (as food additives). In agriculture, the peptide  
CC may be used to improve disease resistance or disease tolerance of crops,  
CC either pre or post harvest. When applied to plants they may also have  
CC curative as well as protective actions. The peptides may also be used to  
CC protect plants by introducing them, or a microorganism capable of  
CC expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct  
CC PI field.)  
XX  
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 6.46e-24 Length: 414  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: Gaps: 0  
US-10-681-972-2 (1-50) x AAT72333 (1-414)  
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 165  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 166 AAGAATCAGTGCATTAACTTGAAGAACGACGACATGGATCTTGCAACTATGCTTCCCA 225  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 226 GCTCACAAAGTGTATCTGACTTCTTCTTGT 255  
RESULT 9  
AAT68696  
ID AAT68696 standard; cDNA; 414 BP.  
XX

ADCS11223 standard; DNA; 426 BP.

ADCS11223; (first entry)

18-DEC-2003 (first entry)

Brassica defensin protein coding sequence.

antimicrobial protein; defensin; transgenic plant;

composite disease resistance; pathogenic bacteria;

rice white leaf blight; brown-stripe disease; glume blight;

seedling damping-off disease; filamentous fungi; rice blight;

sheath blight disease; leaf blight; gene; ds.

Brassica sp.

Key Location/Qualifiers

CDS 1..243

/\*tag= a

/product= "Brassica defensin protein"

JP2003088379-A.

25-MAR-2003.

18-SEP-2001; 2001JP-00283117.

18-SEP-2001; 2001JP-00283117.

(DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

WPI; 2003-621123/59.

P-PSDB; ADCS1224.

Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.

Claim 3; SEQ ID NO 3; 34pp; Japanese.

The invention comprises the amino acid and coding sequences of antimicrobial (defense) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transgenic plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brown-stripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.

Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.69e-24 Length: 426

Score: 283.00 Matches: 45

Percent Similarity: 96.00% Conservative: 3

Best Local Similarity: 90.00% Mismatches: 2

Query Match: 92.79% Indels: 0

DB: Gaps: 0

US-10-681-972-2 (1-50) x ADCS1223 (1-426)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 91 AAGTGTGCGAGAGCCCAAGTGGACATGTCAGGAGTCGTGGAAACAATAACGCATGC 150

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 151 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGGATCTTGCACATATGCTTTCCCA 210

QY 41 AlahisCysCysIleCysTyrPheProCys 50

RESULT 10

Db 211 GCTCACAGTGATTGCTACTTCCCTTGT 240

RESULT 11

ADA68378

ID ADA68378 standard; DNA; 243 BP.

XX AC ADA68378;

XX DT 20-NOV-2003 (first entry)

XX DE Arabidopsis thaliana gene, SEQ ID 747.

XX KW Plant; bacterial infection; fungal infection; viral infection; ds.

XX OS Arabidopsis thaliana.

XX PN WO2003000898-A1.

XX PD 03-JAN-2003.

XX PF 22-JUN-2001; 2001WO-IB001105.

XX PR 22-JUN-2001; 2001WO-IB001105.

XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX DR WPI; 2003-175290/17.

XX FT Identifying at least one gene involved in plant resistance or response to

XX PT pathogenic infection for conferring resistance or tolerance to a plant to

XX PT bacterial, fungal or viral infection by determining or detecting plant

XX PT gene expression.

XX PS Claim 6; SEQ ID NO 747; 899pp; English.

XX CC The present invention relates to a method (M1) for identifying genes

XX CC involved in plant resistance or response to pathogenic infection. M1

XX CC comprises identifying a gene whose expression is significantly altered in

XX CC the incompatible interaction of plant gene expression relative to

XX CC expression of the gene in an uninfected plant, in a mutant plant that

XX CC does not express a gene associated with response to pathogenic infection,

XX CC or in a corresponding incompatible or compatible interaction. (M1) is

XX CC useful for conferring resistance to resistance or tolerance to a plant to

XX CC bacterial, fungal or viral infection. The present sequence was used to

XX CC illustrate the invention.

XX SQ Sequence 243 BP; 58 A; 56 C; 59 G; 70 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.28e-23 Length: 243

Score: 278.00 Matches: 44

Percent Similarity: 96.00% Conservative: 4

Best Local Similarity: 88.00% Mismatches: 2

Query Match: 91.15% Indels: 0

DB: 7 Gaps: 0

US-10-681-972-2 (1-50) x ADA68378 (1-243)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 91 AAGTTGTGGAGAGGCAAGTGGGACATGTCGGAGTTTGGGAAACAGTAAACGGTGC 150

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 151 AAGAATCAGTGCAATTAACTTGAGAAAGCAGCAGATGGATCTTGCAACTATGCTTCCCA 210

QY 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 211 GCTCACAAATGATCTGCTACTTCCCATGT 240

RESULT 12

AAV10632

ID AAV10632 standard; DNA; 403 BP.

XX AC AAV10632;

XX DT 23-JUN-1998 (first entry)

XX DE A. thaliana PDF1.1 DNA.

XX KW Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;

XX KW fungi; ss.

XX OS Arabidopsis thaliana.

XX FH Key Location/Qualifiers

FT CDS 26..268

FT /\*tag= a

FT sig\_peptide 26..113

FT /\*tag= b

FT mat\_peptide 114..265

FT /\*tag= c

FT /product= "PDF1.1"

FT /note= "plant defensin"

XX PN WO9800023-A2.

XX PD 08-JAN-1998.

XX PF 20-JUN-1997; 97WO-GB001672.

XX PR 01-JUL-1996; 96GB-00013753.

XX PA (ZENE ) ZENECA LTD.

XX PI Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras PRG, Manners JM;

XX PI Kazan K;

XX WPI; 1998-086663/08.

XX P-PSDB; AAW40345.

XX FT Protecting plants against pathogens by inducing defensin genes - by

XX FT stimulating ethylene or jasmonate pathways, also new promoter of defensin

XX FT gene from Arabidopsis.

XX PS Disclosure; Fig 1; 72pp; English.

XX CC This sequence encodes the Arabidopsis PDF1.1 gene which is used in a

XX CC novel method for the protection of plants against pathogens which

XX CC involves inducing expression of a plant defensin gene by stimulating the

XX CC jasmonate and/or ethylene pathways. The method is used to induce

XX CC protection against necrotrophic pathogens, specifically fungi and does

XX CC not require cytotoxic or potentially harmful chemicals

XX SQ Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.39e-23 Length: 403

Score: 278.00 Matches: 44

Percent Similarity: 96.00% Conservative: 4

Best Local Similarity: 88.00% Mismatches: 2

Query Match: 91.15% Indels: 0

DB: 2 Gaps: 0

US-10-681-972-2 (1-50) x AAV10632 (1-403)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 116 AAGTTGTGGAGAGGCAAGTGGGACATGTCGGAGTTTGGGAAACAGTAAACGGTGC 175

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 176 AAGAATCAGTGCAATTAACTTGAGAAAGCAGCAGATGGATCTTGCAACTATGCTTCCCA 235



Best Local Similarity: 86.00%  
Query Match: 89.84%  
DB: 2 0  
Mismatches: 3  
Indels: 0  
Gaps: 0

US-10-681-972-2 (1-50) x AAQ70130 (1-288)

QY 1 ArgLeuCysGluArgProSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20  
Db 133 AAGTTGTGCCAAGGCCAAGTGGACATGGTCAGAGTCTGTGGAAACAATACGCGATGC 192  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 193 AAGATCAGTGCATTAGACTTGAGAAAGCAGCAGCATGGATCTTGCAACTATGTCTCCCA 252  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 253 GCTCACAAGTGTATCTGCTACTTTCCTTGT 282

RESULT 15

AAAS3190  
ID AAAS3190 standard; DNA; 449 BP.  
XX AC AAAS3190;  
XX AC  
XX DT 06-OCT-2000 (first entry)  
XX DE Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.  
XX KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;  
XX KW pathogenic microbe; radish; rice blast disease; ds.  
XX OS Raphanus sativus.  
XX PN JP2000116379-A.  
XX PD 25-APR-2000.  
XX PF 09-OCT-1998; 98JP-00288472.  
XX PR 09-OCT-1998; 98JP-00288472.  
XX PA (TOYA-) TOYAMA KEN.  
XX DR WPI: 2000-389821/34.  
XX DR P-PSDB; AAY91117.  
XX PT Isolated DNA from Raphanus sativus used to transform a microbe and a  
PT plant to produce an antibacterial protein used to increase resistance of  
PT rice paddy against pathogenic microbes.  
XX PS Claim 1; Page 4; 7pp; Japanese.  
XX CC The present sequence encodes an antibacterial protein, designated  
CC radishin, isolated from Raphanus sativus (radish). A phage or plasmid  
CC comprising radishin can be used for increasing resistance of paddy and  
CC rice blast disease against pathogenic microbes  
XX SQ Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 7.96e-23 Length: 449  
Score: 274.00 Matches: 43  
Percent Similarity: 94.00% Conservative: 4  
Best Local Similarity: 86.00% Mismatches: 3  
Query Match: 89.84% Indels: 0  
DB: 3 Gaps: 0

US-10-681-972-2 (1-50) x AAAS3190 (1-449)

QY 1 ArgLeuCysGluArgProSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20  
Db 131 AAGTTGTGTGACAGAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAATAATACCGCATGC 190

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 191 AAGATCAGTGCATTGACCTTGAGAAAGCAGCAGCATGGGTCTTGCAACTATGTCTTCCCA 250  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 251 GCTCACAAGTGTATCTGTTATTTCCCTTGT 280

Search completed: May 18, 2004, 20:38:40  
Job time : 300 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: May 18, 2004, 20:26:28 ; Search time 63 Seconds  
(without alignments)  
440.437 Million cell updates/sec

Title: US-10-681-972-2  
Perfect score: 305  
Sequence: 1 RLCSRGTSWGVCGNNAC.....EHGSCNYVPAHKICVYFPC 50

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO spool/US10681972/runat 17052004 151740 4379/app\_query.fasta\_1.199  
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=prc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10681972 @CIGN 1.1.44 @runat 17052004 151740 4379 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPELLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305	100.0	270	1	US-08-627-706-14
2	305	100.0	270	3	US-09-103-489-14
3	305	100.0	270	4	US-09-829-381D-14
4	305	100.0	286	1	US-08-627-706-12
5	305	100.0	286	3	US-09-103-489-12
6	305	100.0	286	4	US-09-829-381D-12
7	296	97.0	500	1	US-08-627-706-9
8	296	97.0	500	3	US-09-103-489-9
9	296	97.0	500	4	US-09-829-381D-9
10	283	92.8	285	1	US-08-627-706-16
11	283	92.8	285	3	US-09-103-489-16
12	283	92.8	285	4	US-09-829-381D-16

13	283	92.8	414	1	US-08-377-687-48
14	283	92.8	414	1	US-08-777-192-48
15	283	92.8	414	3	US-08-971-982-48
16	283	92.8	414	4	US-09-077-951-19
17	283	92.8	414	4	US-09-077-948A-45
18	274	89.8	285	1	US-08-627-706-17
19	274	89.8	285	3	US-09-103-489-17
20	274	89.8	285	4	US-09-829-381D-17
21	274	89.8	288	1	US-08-377-687-58
22	274	89.8	288	1	US-08-777-192-58
23	274	89.8	288	3	US-08-971-982-58
24	273	89.5	308	1	US-08-627-706-5
25	273	89.5	308	3	US-09-103-489-5
26	273	89.5	308	4	US-09-829-381D-5
27	234	76.7	306	1	US-08-627-706-8
28	234	76.7	306	3	US-09-103-489-8
29	234	76.7	306	4	US-09-829-381D-8
30	196	64.3	284	1	US-08-377-687-50
31	196	64.3	284	3	US-08-777-192-50
32	196	64.3	284	4	US-08-971-982-50
33	157	51.5	150	1	US-08-377-687-31
34	157	51.5	150	3	US-08-777-192-31
35	157	51.5	150	4	US-08-971-982-31
36	154	50.5	150	1	US-08-377-687-34
37	154	50.5	150	3	US-08-777-192-34
38	154	50.5	150	4	US-08-971-982-34
39	152	49.8	150	1	US-08-377-687-33
40	152	49.8	150	3	US-08-777-192-33
41	152	49.8	150	4	US-08-971-982-33
42	151.5	49.7	147	1	US-08-377-687-36
43	151.5	49.7	147	3	US-08-777-192-36
44	151.5	49.7	147	4	US-08-971-982-36
45	149	48.9	565	4	US-09-589-733C-6

ALIGNMENTS

RESULT 1

US-08-627-706-14  
; Sequence 14, Application US/08627706  
; Patent No. 5773696  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. 5773696th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/627,706  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21(10700)A  
; TELEPHONE: (314)537-6224  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-627-706-14

Alignment Scores:  
Pred. No.: 9,41e-31 Length: 270  
Score: 305.00 Matches: 50  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-681-972-2 (1-50) x US-08-627-706-14 (1-270)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
DB 109 AGGTTGTGCGAGAGACCAAGTGGGACATGTTGAGGAGTTTGTGGGACCAACATGCGATGC 168  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
DB 169 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATATGTCTTCCCA 228  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
DB 229 GCTCACAATGTATTGTACTTCCCATGT 258

RESULT 2

US-09-103-489-14  
Sequence 14, Application US/09103489  
Patent No. 6215048  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yennie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
STREET: 700 Chesterfield Village Parkway No. 6215048th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,489  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
STRANDEDNESS: single  
TYPE: nucleic acid  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-103-489-14

Alignment Scores:  
Pred. No.: 9,41e-31 Length: 270  
Score: 305.00 Matches: 50  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-681-972-2 (1-50) x US-09-103-489-14 (1-270)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
DB 109 AGGTTGTGCGAGAGACCAAGTGGGACATGTTGAGGAGTTTGTGGGACCAACATGCGATGC 168  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
DB 169 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATATGTCTTCCCA 228  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
DB 229 GCTCACAATGTATTGTACTTCCCATGT 258

RESULT 3

US-09-829-381D-14  
Sequence 14, Application US/09829381D  
Patent No. 6653280  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yennie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control  
TITLE OF INVENTION: Plant Pathogenic Fungi  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/09/829,381D  
CURRENT FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 09/103,489  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 14  
LENGTH: 270  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Plasmid  
US-09-829-381D-14

Alignment Scores:  
Pred. No.: 9,41e-31 Length: 270  
Score: 305.00 Matches: 50  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381D-14 (1-270)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
DB 109 AGGTTGTGCGAGAGACCAAGTGGGACATGTTGAGGAGTTTGTGGGACCAACATGCGATGC 168  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
DB 169 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATATGTCTTCCCA 228  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
DB 229 GCTCACAATGTATTGTACTTCCCATGT 258

RESULT 4

US-08-627-706-12

; Sequence 12, Application US/08627706  
; Patent No. 5773696  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yennie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. 5773696th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/627,706  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21(10700)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6224  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 286 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-627-706-12

Alignment Scores:  
Pred. No.: 1.02e-30 Length: 286  
Score: 305.00 Matches: 50  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-681-972-2 (1-50) x US-08-627-706-12 (1-286)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 117 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCATGC 176

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 177 AGGAACCAATGCAGAAACCTTGAAGAGACAGACACGGATCTTGCACATATGCTTCCCA 236

QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 237 GCTCACAATGTATTGTGTTACTTCCCATGT 266

RESULT 5  
US-09-103-489-12  
; Sequence 12, Application US/09103489  
; Patent No. 6215048  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yennie S.  
; APPLICANT: Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. 6215048th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/103,489  
; FILING DATE: 24-JUN-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 537-6224  
; TELEFAX: (314) 537-6047  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 286 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-09-103-489-12

Alignment Scores:  
Pred. No.: 1.02e-30 Length: 286  
Score: 305.00 Matches: 50  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-681-972-2 (1-50) x US-09-103-489-12 (1-286)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 117 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCATGC 176

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 177 AGGAACCAATGCAGAAACCTTGAAGAGACAGACACGGATCTTGCACATATGCTTCCCA 236

QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 237 GCTCACAATGTATTGTGTTACTTCCCATGT 266

RESULT 6  
US-09-829-381D-12  
; Sequence 12, Application US/09829381D  
; Patent No. 6653280  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yennie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide ALVAFP from Alyssum and Methods for Control  
; Controlling Plant Pathogenic Fungi  
; FILE REFERENCE: 38-21 (10700) C  
; CURRENT APPLICATION NUMBER: US/09/829,381D  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/103,489  
; PRIOR FILING DATE: 1998-06-24



NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 286  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic PCR reaction product  
US-09-829-381D-12

Alignment Scores:  
Pred. No.: 1-02e-30 Length: 286  
Score: 305.00 Matches: 50  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 4

US-10-681-972-2 (1-50) x US-09-829-381D-12 (1-286)

QY 1 ArgLeuCyGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 117 AGCTTGTGGAGAGACCAAGTGGACATGTCAGAGATTGTGGGAACACATGTCATGC 176  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 177 AGGAACCAATGCAGAACCTTGAAGAGAGAGACGATCTTGCACACTATGCTTCCCA 236  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 237 GCTCACAAATGATTGTTACTTCCCATGT 266

RESULT 7

US-08-627-706-9  
Sequence 9, Application US/08627706  
Patent No. 5773696  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
CONTROLLING PLANT PATHOGENIC FUNGI  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
STREET: 700 Chesterfield Village Parkway No. 5773696th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/627,706  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21(10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6224  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
US-08-627-706-9

Alignment Scores:  
Pred. No.: 3.05e-29 Length: 500  
Score: 296.00 Matches: 48  
Percent Similarity: 98.00% Conservative: 1  
Best Local Similarity: 96.00% Mismatches: 1  
Query Match: 97.05% Indels: 0  
Gaps: 1

US-10-681-972-2 (1-50) x US-08-627-706-9 (1-500)

QY 1 ArgLeuCyGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 159 AAGTTGTGGAGAGTCCCAAGTGGACATGTCAGGGTGTGTGGGAATAATAACGATGC 218  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 219 AGGAACCAATGCAGAACCTTGAAGAGAGAGACGATCTTGCACACTATGCTTCCCA 278  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 279 GCTCACAAATGATTGTTACTTCCCATGT 308

RESULT 8

US-09-103-489-9  
Sequence 9, Application US/09103489  
Patent No. 6215048  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
CONTROLLING PLANT PATHOGENIC FUNGI  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
STREET: 700 Chesterfield Village Parkway No. 6215048th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,489  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 500 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-103-489-9  
Alignment Scores:  
Pred. No.: 3.05e-29 Length: 500  
Score: 296.00 Matches: 48  
Percent Similarity: 98.00% Conservative: 1

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Best Local Similarity: 96.00% Mismatches: 1
Query Match: 97.05% Indels: 0
DB: 3 Gaps: 0

US-10-681-972-2 (1-50) x US-09-103-489-9 (1-500)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCGAGATCCAAAGTGGACATGTCAGCGGTGTGGGAATATATACGCATGC 218
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 219 AGGAACCAATGTCAGAACCTTGAAGAGCAGACACGCGATCTTCAACTATGTCTTCCCA 278
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAATGATTATTGTTACTTCCCATGT 308

RESULT 9
US-09-829-381D-9
; Sequence 9, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yinnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyesum and Methods for Controlling Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; TYPE: DNA
; LENGTH: 500
; ORGANISM: Alyesum spp
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22)-(22)
; OTHER INFORMATION: N = any nucleotide
US-09-829-381D-9

Alignment Scores:
Pred. No.: 3,05e-29 Length: 500
Score: 296.00 Matches: 48
Percent Similarity: 98.00% Conservatative: 1
Best Local Similarity: 96.00% Mismatches: 1
Query Match: 97.05% Indels: 0
DB: 4 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381D-9 (1-500)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCGAGATCCAAAGTGGACATGTCAGCGGTGTGGGAATATATACGCATGC 218
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 219 AGGAACCAATGTCAGAACCTTGAAGAGCAGACACGCGATCTTCAACTATGTCTTCCCA 278
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAATGATTATTGTTACTTCCCATGT 308

RESULT 10
US-08-627-706-16
; Sequence 16, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yinnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
```

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; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yinnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) A
; CURRENT APPLICATION NUMBER: US/08/627,706
; CURRENT FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)/A
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-16

Alignment Scores:
Pred. No.: 6.7e-28 Length: 285
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservatative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 1 Gaps: 0

US-10-681-972-2 (1-50) x US-08-627-706-16 (1-285)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGCCATCAGGACTTGGTCAGGAGTCGCGAAACAAACGCGATGC 180
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCATATGTCATCAACCTCGAGAGCGACGCGATGGATCTTGCAACTACGCTTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCACAATGTCATCTGCTACTTTCCATGC 270

RESULT 11
US-09-103-489-16
; Sequence 16, Application US/09103489
; Patent No. 6215046
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yinnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
```

NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
STREET: 700 Chesterfield Village Parkway No. 6215048th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/103,489  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:

LENGTH: 285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-09-103-489-16

Alignment Scores:  
Pred. No.: 6.7e-28 Length: 285  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 3 Gaps: 0

US-10-681-972-2 (1-50) x US-09-103-489-16 (1-285)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 121 AAGTTGTGCGAGAGCCATCAGGGACTTGGTCAGGAGTCTGGGAAACAAACACCATGC 180  
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 181 AAGAACCAATGCATCAACCTCGAGAAGCAGCGCATGGATCTTGCAACTACGCTTCCCA 240  
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

## RESULT 12

US-09-829-381D-16  
Sequence 16, Application US/09829381D  
Patent No. 6653280  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide ALXAPP from Alyseum and Methods for Control  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/09/829,381D  
CURRENT FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 09/103,489  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 285  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-829-381D-16

Alignment Scores:  
Pred. No.: 6.7e-28 Length: 285  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 4 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381D-16 (1-285)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 121 AAGTTGTGCGAGAGCCATCAGGGACTTGGTCAGGAGTCTGGGAAACAAACACCATGC 180  
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 181 AAGAACCAATGCATCAACCTCGAGAAGCAGCGCATGGATCTTGCAACTACGCTTCCCA 240  
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

## RESULT 13

US-08-377-687-48  
Sequence 48, Application US/08377687  
Patent No. 5538525

GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 16..255  
US-08-377-687-48

## Alignment Scores:

Pred. No.: 1.1e-27 Length: 414  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 1 Gaps: 0

US-10-681-972-2 (1-50) x US-08-377-687-48 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20  
Db 106 AAGTTGTGCGAAGGCCCAAGTGGACATGGTCAGAGTCTGTGGAAACATAATACGCATGC 165  
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 166 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA 225  
Qy 41 AlaHisIysCysIleCysTyrPheProCys 50  
Db 226 GCTCACAAGTGTATCTGCTACTTTTCCTTGT 255

## RESULT 14

US-08-777-192-48  
; Sequence 48, Application US/08777192  
; Patent No. 5824869

## GENERAL INFORMATION:

; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, FRANKY R.G.  
; APPLICANT: VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,192  
; FILING DATE:  
; CLASSIFICATION:

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/002,480  
; FILING DATE: 04-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 414 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 16..255  
US-08-777-192-48

## Alignment Scores:

Pred. No.: 1.1e-27 Length: 414  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 1 Gaps: 0

US-10-681-972-2 (1-50) x US-08-777-192-48 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20  
Db 106 AAGTTGTGCGAAGGCCCAAGTGGACATGGTCAGAGTCTGTGGAAACATAATACGCATGC 165  
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 166 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA 225  
Qy 41 AlaHisIysCysIleCysTyrPheProCys 50  
Db 226 GCTCACAAGTGTATCTGCTACTTTTCCTTGT 255

## RESULT 15

US-08-971-982-48  
; Sequence 48, Application US/08971982  
; Patent No. 6187904

## GENERAL INFORMATION:

; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, FRANKY R.G.  
; APPLICANT: VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/971,982  
; FILING DATE: 17-No. 6187904-1997  
; CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/002,480  
; FILING DATE: 04-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 414 base pairs

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;
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-971-982-48

Alignment Scores:
Pred. No.: 1..e-27 Length: 414
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 3 Gaps: 0

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Db 106 AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACCAATAACGCATGC 165
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AGAATCAGTGCATTAACTTGGAGAGCAGCATGGATCTTGGCAACTATGTCTTCCCA 225
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAGGTATCTGCTACTTCTCTTGT 255
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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(without alignments)

785.130 Million cell updates/sec

Title: US-10-681-972-2

Perfect score: 305

Sequence: 1 RLCPSPGTSWGVCGNNAC.....EHGSCNVFFPAHKICVYFPC 50

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Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA.\*

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19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	305	100.0	270	13	US-10-681-972-14	Sequence 14, Appl
3	305	100.0	286	9	US-09-829-381A-12	Sequence 12, Appl
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5	296	97.0	500	9	US-09-829-381A-9	Sequence 9, Appl
6	296	97.0	500	13	US-10-681-972-9	Sequence 9, Appl
7	283	92.8	285	9	US-09-829-381A-16	Sequence 16, Appl
8	283	92.8	285	13	US-10-681-972-16	Sequence 16, Appl
9	283	92.8	414	9	US-09-759-584-48	Sequence 48, Appl
10	283	92.8	414	13	US-10-388-361A-45	Sequence 45, Appl
11	283	92.8	414	14	US-10-006-252A-19	Sequence 19, Appl
12	278	91.1	403	9	US-09-732-561-13	Sequence 13, Appl
13	274	89.8	285	9	US-09-829-381A-17	Sequence 17, Appl
14	274	89.8	288	13	US-10-681-972-17	Sequence 17, Appl
15	274	89.8	288	9	US-09-759-584-58	Sequence 58, Appl
16	273	89.5	308	9	US-09-829-381A-5	Sequence 5, Appl
17	273	89.5	308	13	US-10-681-972-5	Sequence 5, Appl
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20	265	86.9	400	9	US-09-732-561-15	Sequence 15, Appl
21	265	86.9	400	9	US-09-887-576-607	Sequence 607, App
22	265	86.9	1616	9	US-09-732-561-21	Sequence 21, Appl
23	234	76.7	306	9	US-09-829-381A-8	Sequence 8, Appl
24	234	76.7	306	13	US-10-681-972-8	Sequence 8, Appl
25	196	64.3	284	9	US-09-759-584-50	Sequence 50, Appl
26	175	57.4	373	9	US-09-770-696-283	Sequence 283, App
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28	169	55.4	250	15	US-10-178-449A-36	Sequence 36, Appl
29	169	55.4	610	15	US-10-178-449A-29	Sequence 29, Appl
30	169	55.4	658	15	US-10-178-449A-7	Sequence 7, Appl
31	160	52.5	579	15	US-10-178-449A-31	Sequence 31, Appl
32	157	51.5	150	9	US-09-759-584-31	Sequence 31, Appl
33	157	51.5	529	15	US-10-178-449A-48	Sequence 48, Appl
34	154	50.5	150	9	US-09-759-584-34	Sequence 34, Appl
35	153	50.2	439	15	US-10-178-449A-15	Sequence 15, Appl
36	153	50.2	457	15	US-10-178-449A-13	Sequence 13, Appl
37	153	50.2	458	15	US-10-178-449A-21	Sequence 21, Appl
38	153	50.2	460	15	US-10-178-449A-3	Sequence 3, Appl
39	153	50.2	460	15	US-10-178-449A-17	Sequence 17, Appl
40	153	50.2	461	15	US-10-178-449A-46	Sequence 46, Appl
41	153	50.2	463	15	US-10-178-449A-9	Sequence 9, Appl
42	153	50.2	464	15	US-10-178-449A-19	Sequence 19, Appl
43	153	50.2	472	15	US-10-178-449A-23	Sequence 23, Appl
44	153	50.2	503	15	US-10-178-449A-1	Sequence 1, Appl
45	153	50.2	603	15	US-10-178-449A-11	Sequence 11, Appl

## ALIGNMENTS

### RESULT 1

US-09-829-381A-14

; Sequence 14, Application US/09829381A

; Patent No. US20020144306A1

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; Shah, Dilip M.

; Wu, Yonnie S.

; Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for

; Controlling Plant Pathogenic Fungi

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th

; CITY: St. Louis

; STATE: Missouri

; COUNTRY: USA

; ZIP: 63198

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/829,381A  
FILING DATE: 09-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/103,489  
FILING DATE: 1998-06-24  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-829-381A-14

Alignment Scores:  
Pred. No.: 1.27e-33 Length: 270  
Score: 305.00 Matches: 50  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-14 (1-270)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 109 AGGTTGTGGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCATGC 168  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 169 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACCGATCTTGCAACTATGTCTTCCCA 228

QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 229 GCTCACAAATGATTGTTACTTCCCATGT 258

## RESULT 2

US-10-681-972-14  
Sequence 14, Application US/10681972  
Publication No. US20040064850A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Controlling Plant Pathogenic Fungi  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/10/681,972  
CURRENT FILING DATE: 2003-10-09  
PRIOR APPLICATION NUMBER: US/09/829,381D  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 09/103,489  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 14  
LENGTH: 270  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Plasmid

## US-10-681-972-14

Alignment Scores:  
Pred. No.: 1.27e-33 Length: 270  
Score: 305.00 Matches: 50  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-681-972-2 (1-50) x US-10-681-972-14 (1-270)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 109 AGGTTGTGGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCATGC 168  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 169 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACCGATCTTGCAACTATGTCTTCCCA 228  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 229 GCTCACAAATGATTGTTACTTCCCATGT 258

## RESULT 3

US-09-829-381A-12  
Sequence 12, Application US/09829381A  
Patent No. US20020144306A1

## GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip M.

Wu, Yonnie S.

Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF

STREET: 700 Chesterfield Village Parkway No. US20020144306A1

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/829,381A

FILING DATE: 09-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224

TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-829-381A-12

Alignment Scores:

Pred. No.: 1.37e-33 Length: 286  
Score: 305.00 Matches: 50  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-12 (1-286)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
DB 117 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCGATGC 176

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
DB 177 AGGAACCAATGCGAAGAACCTTGAAGAGACGAGACCGATCTTGCAACTATGTCTTCCCA 236

QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
DB 237 GCTCACAATGATTTGTTACTTCCCATGT 266

## RESULT 4

US-10-681-972-12  
; Sequence 12, Application US/10681972  
; Publication No. US20040064850A1  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yennie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Controlling Plant Pathogenic Fungi  
; FILE REFERENCE: 38-21 (10700) C  
; CURRENT APPLICATION NUMBER: US/10/681,972  
; PRIOR FILING DATE: 2003-10-09  
; PRIOR APPLICATION NUMBER: US/09/829,381D  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/103,489  
; PRIOR FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 286  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic PCR reaction product  
US-10-681-972-12

Alignment Scores:  
Pred. No.: 1.37e-33 Length: 286  
Score: 305.00 Matches: 50  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-681-972-2 (1-50) x US-10-681-972-12 (1-286)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
DB 117 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCGATGC 176

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
DB 177 AGGAACCAATGCGAAGAACCTTGAAGAGACGAGACCGATCTTGCAACTATGTCTTCCCA 236

QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
DB 237 GCTCACAATGATTTGTTACTTCCCATGT 266

## RESULT 5

US-09-829-381A-9

; Sequence 9, Application US/09829381A  
; Patent No. US20020144306A1  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yennie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi

; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/829,381A  
; FILING DATE: 09-Apr-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/103,489  
; FILING DATE: 1998-06-24  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 537-6224  
; TELEFAX: (314) 537-6047

; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 500 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-829-381A-9

Alignment Scores:  
Pred. No.: 5.17e-32 Length: 500  
Score: 236.00 Matches: 48  
Percent Similarity: 98.00% Conservative: 1  
Best Local Similarity: 96.00% Mismatches: 1  
Query Match: 97.05% Indels: 0  
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-9 (1-500)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
DB 159 AAGTTGTGCGAGAGTCCAAAGTGGGAACATGTCAGGCGTGTGGGAATAATAACGCGATGC 218

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
DB 219 AGGAACCAATGCGAAGAACCTTGAAGAGACGAGACCGATCTTGCAACTATGTCTTCCCA 278

QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
DB 279 GCTCACAATGATTTGTTACTTCCCATGT 308

## RESULT 6

US-10-681-972-9  
; Sequence 9, Application US/10681972  
; Publication No. US20040064850A1  
; GENERAL INFORMATION:



APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Controlling Plant Pathogenic Fungi  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/10/681,972  
PRIOR FILING DATE: 2003-10-09  
CURRENT FILING DATE: 2003-10-09  
PRIOR FILING DATE: 2001-04-09  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 9  
LENGTH: 500  
TYPE: DNA  
ORGANISM: Alyssum spp  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (22)..(22)  
OTHER INFORMATION: N = any nucleotide  
US-10-681-972-9

Alignment Scores:  
Pred. No.: 517e-32 Length: 500  
Score: 296.00 Matches: 48  
Percent Similarity: 98.00% Conservative: 1  
Best Local Similarity: 96.00% Mismatches: 1  
Query Match: 97.05% Indels: 0  
DB: 13 Gaps: 0

US-10-681-972-2 (1-50) x US-10-681-972-9 (1-500)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 159 AAGTTGTGCGAGAGTCCCAAGTGGACATGGTCAGCGTGTGGTGGATATAACGCATGC 218  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 219 AGGAACCAATGACGAACCTTGAAGAGCAGACACGCGATCTTGCACACTATGTCTTCCCA 278  
QY 41 AlaHisLysCysLleCysTyrPheProCys 50  
Db 279 GCTCACAAATGATTTGTTACTTCCATGT 308

RESULT 7  
US-09-829-381A-16  
Sequence 16, Application US/09829381A  
Publication No. US20020144306A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESS: Charles E. Cohen, Monsanto Company, BB4F  
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/829,381A

APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Controlling Plant Pathogenic Fungi  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/10/681,972  
PRIOR FILING DATE: 2003-10-09  
CURRENT FILING DATE: 2003-10-09  
PRIOR FILING DATE: 2001-04-09  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 16  
LENGTH: 285  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-681-972-16

FILING DATE: 09-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/103,489  
FILING DATE: 1998-06-24  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-829-381A-16

Alignment Scores:  
Pred. No.: 1.66e-30 Length: 285  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-16 (1-285)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 121 AAGTTGTGCGAGAGTCCCAAGTGGACATGGTCAGCGTGTGGTGGATATAACGCATGC 180  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 181 AAGAACCAATGACATCAACCTCGAGAGCGCAGCGATCTTGCACACTAGTCTTCCCA 240  
QY 41 AlaHisLysCysLleCysTyrPheProCys 50  
Db 241 GCTCACAAATGATCTGCTACTTCCATGC 270

RESULT 8  
US-10-681-972-16  
Sequence 16, Application US/10681972  
Publication No. US20040064850A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Controlling Plant Pathogenic Fungi  
FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/10/681,972  
PRIOR FILING DATE: 2003-10-09  
CURRENT FILING DATE: 2003-10-09  
PRIOR FILING DATE: 2001-04-09  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 16  
LENGTH: 285  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-681-972-16

Alignment Scores: 1.66e-30 Length: 285  
Pred. No.: 283.00 Matches: 45  
Score: 96.00% Conservative: 3  
Percent Similarity: 96.00% Mismatches: 2  
Best Local Similarity: 90.00% Indels: 0  
Query Match: 92.79% Gaps: 0  
DB: 13

US-10-681-972-2 (1-50) x US-10-681-972-16 (1-285)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 121 AAGTTGTGCGAGGCAATCAGGACTTGTTCAGGAGTCTGTGCGAACAACACCGCATGC 180  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 181 AAGAACCATGATCAACCTCGAGAGGACGCGCATGGATCTTGCACACTACGCTCTCCCA 240  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 241 GCTCACAAGTGCATCTGCTACTTTCCTTGT 270

RESULT 9

US-09-759-584-48  
; Sequence 48, Application US/09759584  
; Patent No. US20010014732A1  
; GENERAL INFORMATION:  
; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, FRANKY R.G.  
; APPLICANT: VANDERLEIDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARB & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/759,584  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/377,687  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 414 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 16..255  
; US-09-759-584-48

Alignment Scores: 2.69e-30 Length: 414  
Pred. No.: 283.00 Matches: 45  
Score: 96.00% Conservative: 3  
Percent Similarity: 96.00% Mismatches: 2  
Best Local Similarity: 90.00% Indels: 0  
Query Match: 92.79% Gaps: 0  
DB: 9

US-10-681-972-2 (1-50) x US-09-759-584-48 (1-414)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 106 AAGTTGTGCGAAGGCAATGCGACATGTCAGGAGTCTGTGGAACAATAACGCAIGC 165  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 166 AAGATCATGTCATTAACTTGGAGAAGACGACATGGATCTTGCACACTATGCTTCCCA 225  
QY 41 AlaHisLysCysIleCysTyrPheProCys 50  
Db 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 10

US-10-388-361A-45  
; Sequence 45, Application US/10388361A  
; Publication No. US20030226169A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Amerongen, Aart  
; APPLICANT: Fant, Franky  
; APPLICANT: Borremans, Frans  
; APPLICANT: De Samblanx, Geneveva  
; APPLICANT: Sitjtsma, Lolke  
; APPLICANT: Meloen, Robbert  
; APPLICANT: Buijk, Wouter  
; APPLICANT: Schaaper, Wilhelmus  
; APPLICANT: Broekaert, Willem  
; APPLICANT: Van Gelder, Wilhelms  
; APPLICANT: Rees, Sarah  
; TITLE OF INVENTION: Antifungal Proteins  
; FILE REFERENCE: 50094PPDDIV  
; CURRENT APPLICATION NUMBER: US/10/388,361A  
; CURRENT FILING DATE: 2003-03-13  
; PRIOR APPLICATION NUMBER: US 09/077,948  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: PCT/GB96/03068  
; PRIOR FILING DATE: 1996-12-12  
; PRIOR APPLICATION NUMBER: GB 9606552.9  
; PRIOR FILING DATE: 1996-03-28  
; PRIOR APPLICATION NUMBER: GB 9525455.3  
; PRIOR FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 414  
; TYPE: DNA  
; ORGANISM: Raphanus sativus  
; US-10-388-361A-45

Alignment Scores: 2.69e-30 Length: 414  
Pred. No.: 283.00 Matches: 45  
Score: 96.00% Conservative: 3  
Percent Similarity: 96.00% Mismatches: 2  
Best Local Similarity: 90.00% Indels: 0  
Query Match: 92.79% Gaps: 0  
DB: 13

US-10-681-972-2 (1-50) x US-10-388-361A-45 (1-414)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 106 AAGTTGTGCGAAGGCAATGCGACATGTCAGGAGTCTGTGGAACAATAACGCAIGC 165  
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAATCAGTGCATTAACCTTGAGAAAGACGACATGGATCTTGCAACTATGCTTCCCA 225

Qy 41 AlahisLysCysIleCysTyrPheProCys 50  
Db 226 GCTCACAAGTGATCTGCTACTTTCCTGT 255

RESULT 11  
US-10-006-252A-19  
; Sequence 19, Application US/10006252A  
; Publication No. US20020152498A1  
; GENERAL INFORMATION:  
; APPLICANT: De Samblanx, Genoveva  
; APPLICANT: Broekaert, Willem  
; APPLICANT: Rees, Sarah  
; TITLE OF INVENTION: Antifungal Proteins  
; FILE REFERENCE: SYN-034DV  
; CURRENT APPLICATION NUMBER: US/10/006,252A  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 09/077,951  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: GB 9525474.4  
; PRIOR FILING DATE: 1995-12-13  
; PRIOR APPLICATION NUMBER: PCT/GB96/03065  
; PRIOR FILING DATE: 1996-12-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 414  
; TYPE: DNA  
; ORGANISM: Raphanus sativus  
US-10-006-252A-19

Alignment Scores:  
Pred. No.: 2,69e-30 Length: 414  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x US-10-006-252A-19 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 106 AAGTTGTGCGAAGAGCCAGTGGGACATGTCAGAGTCTGTGGAACATATACGCATGC 165  
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 166 AAGAATCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTCCCA 225  
Qy 41 AlahisLysCysIleCysTyrPheProCys 50  
Db 226 GCTCACAAGTGATCTGCTACTTTCCTGT 255

RESULT 12  
US-09-732-561-13  
; Sequence 13, Application US/09732561  
; Patent No. US20020035738A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomma, Bart  
; APPLICANT: Terras, Franky  
; APPLICANT: Penninckx, Iris  
; APPLICANT: Manners, John  
; APPLICANT: Kazan, Kemal  
; APPLICANT: Broekaert, Willem  
; TITLE OF INVENTION: Plant Protection Method  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZENECA Ag Products  
; STREET: 1800 Concord Pike  
; CITY: Wilmington  
; STATE: DE

COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/732,561  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/202,638  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB97/01672  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: PPD 50165/UST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-1699  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 403 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
STRAIN: PDF 1.1  
US-09-732-561-13

Alignment Scores:  
Pred. No.: 1.3e-29 Length: 403  
Score: 279.00 Matches: 44  
Percent Similarity: 96.00% Conservative: 4  
Best Local Similarity: 88.00% Mismatches: 2  
Query Match: 91.15% Indels: 0  
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-732-561-13 (1-403)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
Db 116 AAGTTGTGCGAGAGCCAGTGGGACATGTCGGAGTTTGGGAAACAGTAACGCCTGC 175  
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
Db 176 AAGAATCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTCCCA 235  
Qy 41 AlahisLysCysIleCysTyrPheProCys 50  
Db 236 GCTCACAAGTGATCTGCTACTTTCCTGT 265

RESULT 13  
US-09-829-381A-17  
; Sequence 17, Application US/09829381A  
; Patent No. US20020144306A1  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1ch  
; CITY: St. Louis  
; STATE: Missouri

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; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-381A-17

Alignment Scores:
Pred. No.: 3,02e-29 Length: 285
Score: 274.00 Matches: 43
Percent Similarity: 94.00% Conservative: 4
Best Local Similarity: 86.00% Mismatches: 3
Query Match: 89.84% Indels: 0
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-17 (1-285)
QY 1 ArgLeuGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 20
Db 121 AAGTTGTGCCAAGGCCATCAGGAGCTTGGTCAGGAGTCTGGGAAACACACACGCGATGC 180
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAGACTCGAAGAGGCACGCGATGGATCTTGCAACTACGCTCTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCAAGTGCATCTGCTACTTCCATGC 270

RESULT 14
US-10-681-972-17
; Sequence 17, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alysium and Methods for Control
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; CURRENT FILING DATE: 2003-10-09
; PRIORITY INFORMATION:
; PRIORITY NUMBER: US/09/829,381D
; PRIORITY DATE: 2001-04-09
; PRIORITY APPLICATION NUMBER: 09/103,489
; PRIORITY FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20

; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-381A-17

Alignment Scores:
Pred. No.: 3,02e-29 Length: 285
Score: 274.00 Matches: 43
Percent Similarity: 94.00% Conservative: 4
Best Local Similarity: 86.00% Mismatches: 3
Query Match: 89.84% Indels: 0
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-17 (1-285)
QY 1 ArgLeuGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 20
Db 121 AAGTTGTGCCAAGGCCATCAGGAGCTTGGTCAGGAGTCTGGGAAACACACACGCGATGC 180
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAGACTCGAAGAGGCACGCGATGGATCTTGCAACTACGCTCTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCAAGTGCATCTGCTACTTCCATGC 270

RESULT 15
US-09-759-584-58
; Sequence 58, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKI R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-681-972-17

Alignment Scores:
Pred. No.: 3,02e-29 Length: 285
Score: 274.00 Matches: 43
Percent Similarity: 94.00% Conservative: 4
Best Local Similarity: 86.00% Mismatches: 3
Query Match: 89.84% Indels: 0
DB: 13 Gaps: 0

US-10-681-972-2 (1-50) x US-10-681-972-17 (1-285)
QY 1 ArgLeuGlnCysArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCCAAGGCCATCAGGAGCTTGGTCAGGAGTCTGGGAAACACACACGCGATGC 180
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAGACTCGAAGAGGCACGCGATGGATCTTGCAACTACGCTCTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCAAGTGCATCTGCTACTTCCATGC 270

RESULT 15
US-09-759-584-58
; Sequence 58, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKI R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
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;  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 43..282  
; US-09-759-584-58

Alignment Scores:  
Pred. No.: 3.06e-29 Length: 288  
Score: 274.00 Matches: 43  
Percent Similarity: 94.00% Conservative: 4  
Best Local Similarity: 86.00% Mismatches: 3  
Query Match: 89.84% Indels: 0  
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-759-584-58 (1-288)

QY	1	ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys	20
Db	133	AAATTGTGCCAAAGGCCAAGTGGGACATGTCAGGAGTCGTGGAAACACATAACGCATGC	192
QY	21	ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro	40
Db	193	AAAGATCAGTGCATTAGACTTGAGAAAGCAGCAGCATGGATCTTGCAACTATGCTTCCCA	252
QY	41	AlaHisLysCysIleCysTyrPheProCys	50
Db	253	GCTCACAGTGATCTGCTACTTCTCTTGT	282

Search completed: May 18, 2004, 22:55:50  
Job time : 290 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 18, 2004, 20:22:48 ; Search time 2363 Seconds  
(without alignments)  
631.870 Million cell updates/sec

Title: US-10-681-972-2

Perfect score: 305

Sequence: 1 RLCERSGTFWSGVCNNAC.....EHGSCNVVFFAHKICVFC 50

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2/1/USPTO.spool/US10681972/runat.17052004.151740.4363/app.query.fasta.1.199  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est6:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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4	283	92.8	419	14	CD834168	CD834168 BN45.040N
5	283	92.8	420	14	CD833944	CD833944 BN45.040B
6	283	92.8	421	14	CD826491	CD826491 BN25.064A
7	283	92.8	421	14	CD831111	CD831111 BN40.058A
8	283	92.8	421	14	CD833977	CD833977 BN45.040D
9	283	92.8	422	14	CD833983	CD833983 BN45.040D
10	283	92.8	426	14	CD827413	CD827413 BN25.067G
11	283	92.8	438	14	CD831294	CD831294 BN40.058N
12	283	92.8	438	14	CD831479	CD831479 BN40.059J
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14	283	92.8	447	14	CD832592	CD832592 BN40.063O
15	283	92.8	450	14	CD834611	CD834611 BN45.042H
16	283	92.8	452	14	CD832071	CD832071 BN40.061O
17	283	92.8	453	14	CD834008	CD834008 BN45.040E
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19	283	92.8	470	14	CD831680	CD831680 BN40.060H
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21	283	92.8	553	14	CD831014	CD831014 BN40.047K
22	283	92.8	803	28	BH458392	BH458392 BOCWE36TF
23	279	91.5	422	14	CD831972	CD831972 BN40.061I
24	278	91.1	318	9	AA713157	AA713157 32717 Lam
25	278	91.1	394	12	BG321454	BG321454 DS01.08H0
26	278	91.1	421	9	AV816118	AV816118 AV816118
27	278	91.1	422	9	AV787956	AV787956 AV787956
28	277	90.8	409	14	CD832294	CD832294 BN40.062L
29	277	90.8	425	14	CD834852	CD834852 BN45.043G
30	277	90.8	427	14	CD833613	CD833613 BN40.067P
31	277	90.8	449	14	CD833047	CD833047 BN40.065M
32	277	90.8	457	14	CD831226	CD831226 BN40.058J
33	277	90.8	473	14	CD834995	CD834995 BN45.043O
34	277	90.8	476	14	CD833784	CD833784 BN45.001I
35	277	90.8	476	14	CD834092	CD834092 BN45.040I
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37	277	90.8	482	14	CD833627	CD833627 BN45.001A
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39	277	90.8	543	14	CD828840	CD828840 BN40.040A
40	277	90.8	543	14	CD830628	CD830628 BN40.046D
41	277	90.8	645	14	CD829429	CD829429 BN40.042B
42	277	90.8	762	28	BZ517729	BZ517729 BOMSG66TF
43	274	89.8	421	14	CD837517	CD837517 BN45.052I
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# ALIGNMENTS

RESULT 1  
CD833779  
LOCUS CD833779 408 bp mRNA linear EST 10-JUL-2003  
DEFINITION BN45.001115F010914 BN45 Brassica napus cDNA clone BN45001115, mRNA sequence.  
ACCESSION CD833779  
VERSION CD833779.1 GI:32515719  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

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REFERENCE
1 (bases 1 to 408)
Genoplante.
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040121"
/tissue_type="seed"
/clone_lib="BN45"
ORIGIN
Alignment Scores:
Pred. No.: 7.23e-22 Length: 408
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0
US-10-681-972-2 (1-50) x CD833779 (1-408)
QY 1 ArgLeuCysGluArgProSerGlyThrTTPSerGlyValCysGlyAsnAsnAlaCys 20
Db 118 AGTTGTGGAGAGGCCAAGTGGGACATGTCAGGAGTCTGCGAAGCAATACGCGATGC 177
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 178 AAGATCAGTGCATTAACTTGAAGAACGACGACATGATCTTGCACATATGCTTTCCCA 237
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 238 GCTCACAAGTATTGCTACTTCCCTTGT 267
RESULT 2
CD834090 409 bp mRNA linear EST 10-JUL-2003
LOCUS
DEFINITION
BN45.040121F011018 BN45 Brassica napus cDNA clone BN45040121, mRNA
sequence.
ACCESSION
CD834090
VERSION
CD834090.1 GI:32516030
KEYWORDS
Brassica napus (rape)
SOURCE
Brassica napus
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 409)
AUTHORS
Genoplante.
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.
FEATURES
Location/Qualifiers
1..409
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040121"
/tissue_type="seed"
/clone_lib="BN45"
ORIGIN
Alignment Scores:
Pred. No.: 7.48e-22 Length: 418
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0
US-10-681-972-2 (1-50) x CD834090 (1-409)
QY 1 ArgLeuCysGluArgProSerGlyThrTTPSerGlyValCysGlyAsnAsnAlaCys 20
Db 119 AGTTGTGGAGAGGCCAAGTGGGACATGTCAGGAGTCTGCGAAGCAATACGCGATGC 178
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 179 AAGATCAGTGCATTAACTTGAAGAACGACGACATGATCTTGCACATATGCTTTCCCA 238
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 239 GCTCACAAGTATTGCTACTTCCCTTGT 268
RESULT 3
CD832625 418 bp mRNA linear EST 10-JUL-2003
LOCUS
DEFINITION
BN40.064A14F011227 BN40 Brassica napus cDNA clone BN40064A14, mRNA
sequence.
ACCESSION
CD832625
VERSION
CD832625.1 GI:32514565
KEYWORDS
Brassica napus (rape)
SOURCE
Brassica napus
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 418)
AUTHORS
Genoplante.
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://www.genoplante.com.
FEATURES
Location/Qualifiers
1..418
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40064A14"
/tissue_type="seed"
/clone_lib="BN40"
ORIGIN
Alignment Scores:
Pred. No.: 7.48e-22 Length: 418
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0

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US-10-681-972-2 (1-50) x CD832625 (1-418)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 143 AAGTTGCGAGAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 202
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 203 AAGAATCAGTGCATTAACTTGTGGAAGACGACATGATCTTGCACATATGCTTCCCA 262
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 263 GCTCACAAAGTGATTGCTACTTCCCTTGT 292

RESULT 4
CD834168
LOCUS
DEFINITION
BN45.040N06F011018 BN45 Brassica napus cDNA clone BN45040N06, mRNA
sequence.
ACCESSION
CD834168
VERSION
CD834168.1 GI:32516108
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 419)
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..419
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040N06"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores:
Pred. No.: 7,51e-22 Length: 419
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0
US-10-681-972-2 (1-50) x CD834168 (1-419)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 140 AAGTTGCGAGAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 199
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 200 AAGAATCAGTGCATTAACTTGTGGAAGACGACATGATCTTGCACATATGCTTCCCA 259
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 260 GCTCACAAAGTGATTGCTACTTCCCTTGT 289

RESULT 5
CD833944
LOCUS
DEFINITION
BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
sequence.
ACCESSION
CD833944
VERSION
CD833944.1 GI:32515884
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 420)
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..420
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040B07"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores:
Pred. No.: 7,53e-22 Length: 420
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0
US-10-681-972-2 (1-50) x CD833944 (1-420)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 140 AAGTTGCGAGAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 199
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 200 AAGAATCAGTGCATTAACTTGTGGAAGACGACATGATCTTGCACATATGCTTCCCA 259
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 260 GCTCACAAAGTGATTGCTACTTCCCTTGT 289

RESULT 6
CD826491
LOCUS
DEFINITION
BN25.064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA
sequence.
ACCESSION
CD826491
VERSION
CD826491.1 GI:32508431
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 421)
AUTHORS
Genoplante.

```



This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

Best Local Similarity:	90.00%
Query Match:	92.79%
DB:	14
Miss	
Ind	
Gap	

QY	21	ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTrpValPhePro	40
	:	:	:
Db	201	AGAAGATCAAGTGAATTAACTTGAAAAACAGCATGGATCTTGGAACTAATGCTCCCA	260

RESULT 8	CD833977	LOCUS	421 bp	mRNA	linear	EST 10-JUN-2003
		DEFINITION	BN45.040D05F011019	BN45	<i>Brassica napus</i> cDNA clone BN45040D05, mRNA sequence.	

AUTHORS	TITLE	JOURNAL	COMMENT
genoplatte.	genoplatte, a major partnership french program in plant genomics	Unpublished (2003)	
Contact: Genoplatte			
Genoplatte			
93, rue Henri Rochefort 91025 EVRY CEDEX France			
Tel: 33 1 69 47 54 00			
Fax: 33 1 69 47 54 10			

```

/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN4504DD05"
/tissue_type="seed"
/clone_lib="BN45"

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```

Best Local Similarity: 90.00%
Query Match: 92.79%
DB: 14
Gap: 1
US-10-681-972-2 (1-50) x CD833977 (1-421)

```

```

QY      1  ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141    AAGTTGTGCGAGAGGCCAAGTGGACATGTCAGAGTCTGTGGAAACAATAACGCATGC 200
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201    AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGATCTTGCAACTATGCTTCCCA 260

QY      41  AlahisLysCysIleCysTyrPheProCys 50
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
261    GCTCACAGTGTATTGCTACTTCCCTTGT 290

RESULT 9
CD833983
LOCUS      CD833983               422 bp    mRNA    linear    EST 10-JUL-2003
DEFINITION BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA
sequence.
ACCESSION CD833983
VERSION    CD833983.1 GI:32515923
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 422)
AUTHORS   Genoplatne, a major partnership french program in plant genomics
TITLE     Unpublished (2003)
JOURNAL
COMMENT    Contact: Genoplatne
           Genoplatne
           93, rue Henri Rochefort 91025 EVRY CEDEX France
           Tel: 33 1 69 47 54 00
           Fax: 33 1 69 47 54 10
           This sequence has been generated in the framework of the french
           plant genomics programme 'Genoplatne' (http://www.genoplatne.com)
           and http://genoplatne-info.infobiogen.fr.

FEATURES             source
     source           1..422
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Jet neuf"
                     /db_xref="taxon:3708"
                     /clone="BN45040D11"
                     /tissue_type="seed"
                     /clone_lib="BN45"

ORIGIN
Alignment Scores:
Pred. No.:          7.59e-22          Length:          422
Score:              283.00            Matches:         45
Percent Similarity: 96.00%            Conservative:    3
Best Local Similarity: 90.00%          Mismatches:     2
Query Match:        92.79%            Indels:         0
DB:                 14                Gaps:          0

US-10-681-972-2 (1-50) x CD833983 (1-422)

QY      1  ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141    AAGTTGTGCGAGAGGCCAAGTGGACATGTCAGAGTCTGTGGAAACAATAACGCATGC 200
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201    AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGATCTTGCAACTATGCTTCCCA 260

QY      41  AlahisLysCysIleCysTyrPheProCys 50
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
261    GCTCACAGTGTATTGCTACTTCCCTTGT 290

RESULT 10
CD827413
LOCUS      CD827413               426 bp    mRNA    linear    EST 10-JUL-2003
DEFINITION BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
sequence.
ACCESSION CD827413
VERSION    CD827413.1 GI:32509353
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 426)
AUTHORS   Genoplatne, a major partnership french program in plant genomics
TITLE     Unpublished (2003)
JOURNAL
COMMENT    Contact: Genoplatne
           Genoplatne
           93, rue Henri Rochefort 91025 EVRY CEDEX France
           Tel: 33 1 69 47 54 00
           Fax: 33 1 69 47 54 10
           This sequence has been generated in the framework of the french
           plant genomics programme 'Genoplatne' (http://www.genoplatne.com)
           and http://genoplatne-info.infobiogen.fr.

FEATURES             source
     source           1..426
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Jet neuf"
                     /db_xref="taxon:3708"
                     /clone="BN25067G02"
                     /tissue_type="seed"
                     /clone_lib="BN25"

ORIGIN
Alignment Scores:
Pred. No.:          7.69e-22          Length:          426
Score:              283.00            Matches:         45
Percent Similarity: 96.00%            Conservative:    3
Best Local Similarity: 90.00%          Mismatches:     2
Query Match:        92.79%            Indels:         0
DB:                 14                Gaps:          0

US-10-681-972-2 (1-50) x CD827413 (1-426)

QY      1  ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141    AAGTTGTGCGAGAGGCCAAGTGGACATGTCAGAGTCTGTGGAAACAATAACGCATGC 200
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201    AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGATCTTGCAACTATGCTTCCCA 260

QY      41  AlahisLysCysIleCysTyrPheProCys 50
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
261    GCTCACAGTGTATTGCTACTTCCCTTGT 290

RESULT 11
CD831294
LOCUS      CD831294               438 bp    mRNA    linear    EST 10-JUL-2003
DEFINITION BN40.058N13F011019 BN40 Brassica napus cDNA clone BN40058N13, mRNA
sequence.
ACCESSION CD831294
VERSION    CD831294.1 GI:32513234
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 438)
AUTHORS   Genoplatne, a major partnership french program in plant genomics
TITLE     Unpublished (2003)
JOURNAL

```

## COMMENT

Contact: Genoplatte  
Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

## FEATURES

source  
1..438  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet neuf"  
/db\_xref="taxon:3708"  
/clone="BN40059J13"  
/tissue\_type="seed"  
/clone\_lib="BN40"

## ORIGIN

Alignment Scores:  
Pred. No.: 7,99e-22 Length: 438  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x CD831294 (1-438)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
:::|||||  
DB 141 AAGTTGTCGGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATAACGATGC 200  
21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
:::|||||  
DB 201 AAGATCAGTCATTAACTTGAGAAAGCAGCAGATGATCTTGCAACTATGCTTCCCA 260  
41 AlaHisLysCysIleCysTyrPheProCys 50  
:::|||||  
DB 261 GCTCACAAGTGATTGCTACTTCCCTTGT 290

## RESULT 12

CD831479  
LOCUS  
DEFINITION  
CD831479 438 bp mRNA linear EST 10-JUL-2003  
BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA  
sequence.

ACCESSION  
CD831479

VERSION  
CD831479.1 GI:32513419

KEYWORDS  
EST.

SOURCE  
Brassica napus (rape)

## ORGANISM

Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 438)

Genoplatte.

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

## FEATURES

source  
1..438  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet neuf"  
/db\_xref="taxon:3708"  
/clone="BN40059J13"

/tissue\_type="seed"  
/clone\_lib="BN40"

## ORIGIN

Alignment Scores:  
Pred. No.: 7,99e-22 Length: 438  
Score: 283.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x CD831479 (1-438)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20  
:::|||||  
DB 141 AAGTTGTCGGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATAACGATGC 200  
21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40  
:::|||||  
DB 201 AAGATCAGTCATTAACTTGAGAAAGCAGCAGATGATCTTGCAACTATGCTTCCCA 260  
41 AlaHisLysCysIleCysTyrPheProCys 50  
:::|||||  
DB 261 GCTCACAAGTGATTGCTACTTCCCTTGT 290

## RESULT 13

CD834068  
LOCUS  
DEFINITION  
CD834068 446 bp mRNA linear EST 10-JUL-2003  
BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA  
sequence.

ACCESSION  
CD834068

VERSION  
CD834068.1 GI:32516008

KEYWORDS  
EST.

SOURCE  
Brassica napus (rape)

## ORGANISM

Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 446)

Genoplatte.

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

## FEATURES

source  
1..446  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet neuf"  
/db\_xref="taxon:3708"  
/clone="BN45040H17"  
/tissue\_type="seed"  
/clone\_lib="BN45"

## ORIGIN

Alignment Scores:  
Pred. No.: 8,19e-22 Length: 446  
Score: 289.00 Matches: 45  
Percent Similarity: 96.00% Conservative: 3  
Best Local Similarity: 90.00% Mismatches: 2  
Query Match: 92.79% Indels: 0  
DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x CD834068 (1-446)

QY

1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

```

Db      156 AAGTTGTGCGAGAGCCAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 215
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      216 AAGAATCATGTCATTAACTTGGAGAACGACACATGGATCTTGCAACTATGTCTTCCCA 275
QY      41  AlaHisLysCysIleCysTyrPheProCys 50
Db      276 GCTCAAGTGTATTGTCTACTTCCCTTGT 305

RESULT 14
LOCUS   CD832592
DEFINITION BN40.063015F011228 BN40 Brassica napus cDNA clone BN40063015, mRNA
sequence.
ACCESSION CD832592
VERSION   CD832592.1
KEYWORDS EST.
SOURCE    Brassica napus (rape)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 447)
AUTHORS   Genoplante, a major partnership french program in plant genomics
TITLE     Genoplante.
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..447
/organism="Brassica napus"
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Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x CD832592 (1-447)

QY      1  ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db      155 AAGTTGTGCGAGAGCCAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 214
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      215 AAGAATCATGTCATTAACTTGGAGAACGACACATGGATCTTGCAACTATGTCTTCCCA 274
QY      41  AlaHisLysCysIleCysTyrPheProCys 50
Db      275 GCTCAAGTGTATTGTCTACTTCCCTTGT 304

RESULT 15
LOCUS   CD834611
DEFINITION BN45.042H07F011228 BN45 Brassica napus cDNA clone BN45042H07, mRNA
sequence.
ACCESSION CD834611
VERSION   CD834611.1
KEYWORDS EST.
SOURCE    Brassica napus (rape)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 450)
AUTHORS   Genoplante, a major partnership french program in plant genomics
TITLE     Genoplante.
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
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US-10-681-972-2 (1-50) x CD834611 (1-450)

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QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      216 AAGAATCATGTCATTAACTTGGAGAACGACACATGGATCTTGCAACTATGTCTTCCCA 275
QY      41  AlaHisLysCysIleCysTyrPheProCys 50
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Search completed: May 18, 2004, 21:54:56
Job time : 2364 secs

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